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rson, J.E., Sudok, P.W., Harra, M.C., Cottob, M.D., Scherts, K.M., Hurst, M.A., Schence 273, 1058-1073, 1946.
A:Authors: Kaine P.P.; Perrodomsky M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A.Fittle: Complete geneme seggence of the methanogenic archamon, Methanochoms januarchi A:Reference number: A64300; MUID:9637999; PMID:8688087
A:Authors: Hunter, J.L.: Jenkins, J.: Johnson-Hopson, C.: Khan, S.: Khaykin, E.: Kim, C.C.A.: Li, J.H.: Li, Y.: Lin, X.: Liu, S.X.: Liu, Z.A.: Luros, J.S.: Maiti, R.: Marziali, R.: Rochey, T.: Rowley, D.: Sakano, H.
A:Authors: Salztery, S.L.: Schwartz, J.R.: Shinn, P.: Southwick, A.M.: Sun, H.: Tallon, Ker, M.: Wu. D.: Yu. G.: Fraser, C.M.: Venter, J.C.: Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141: MUID:21016719: PMID:11130712
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A:Title: Deciphering the biology of Myssbacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: R70888
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R:Cole, S.T.; Brosch R: Parkhill J: Garnier, T: Churcher, C:: Harris, L:: Gordun, S:: Connor. R: Devies, R:: Devlin, K:: Feltwell, T:: Genties, S:: Hamlin, N.; Hoirbyd, S:: Rajandream, M.A:: Rogers, J:: Rutter, S:: Seeger, K:: Skelton, S:: Squares, S:
Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Accession: A95595
R:Theologis: A.: Ecker, J.R.: Palm, C.J.: Federspiel, N.A.: Kaul, S.: White, O.: Alonso.
Chin, C.W.: Chung, M.K.: Conn, L.: Conway, A.B.: Conway, A.R.: Creasy, T.H.; Dewar, K.:
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C:Species: Methanococcus jannaschii
C:Dath- 11-Sep-1996 #sequence_revision 12-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                      Chin. C.W.: Chung. M.K.: Conn. L.: ansen. N.F.: Hughes. B.: Huizar, L. Nature 408. 816-820, 2000
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C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T1813 2 [imported] - Arabidopsis thaliana
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Local Similarity 100.0%; Pred. No. 1.3e+02;
hes 5; Conservative 0; Mismatches 0;
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R.; Kirkness, E.F.; Weinstock, K.O.; Merrick, J.M.; O.
Hinda, M.C.; Outton, M.D.; Pukeits, K.M.; Huist, M.A.
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Merrick, JM; Glodek, A.
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Astitle: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid Asperence number: 216408; MUID:9963795; PMID:9847077 Astatus: translated from GB/EMB:/FLBJ A.Molecule type: DNA A.Residues: 1:379 <NGN-A.Residues: 1:379 <NGN-A.Residues
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Genome Res. 8, 1131-1141, 1998
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A:Status: preliminary
A:Melecule type: DNA
A:Residues: 1-354 <STO>
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A:Accession TOR
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C:Date: 11-Jun-1999 #se
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C;Superfamily: carotenoid biosynthesis protein homolog
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Search completed: April 8, 2004, Job time : 26,0833 secs
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A:Gene: pls:
C:Superfamily: mouse l-acylolycerol-3-ph
C:Keywords: acyltransferase: coenzyme A
                                                                                                                                                                                        A:Molecule type: DNA
A:Residues: 1-237 <ARNS
A:Cross-reterences: GB:AED01550: GB:AED01439: NID:q4155872; PIDN:AAD06852.1; PID:q415588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: mFNA
A:Residues: 1-227 <SPE>
A:Cross-reterences: EMBJ:X77575; NID:g482918; PID:g1345528
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Acression: $44281
R:Speulman, E.: Salamini, F.
submitted to the EMBL Data Library, February 1994
                                                                                                                                                                         A:Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                     A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A:Reference number: A71800: MUID:09120557; PMID:0923632 A;Accession: B71827
                                                                                                                                                                                                                                                                                                                                                                                                R:Alm, R.A.: Ling, L.S.L.: Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C., Gibson, R., Methery, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #fext_change 06-Oct-2000
C:Accession: B71827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross_references: DDBJ:AP000064: NID:45105945, FIDN.BAA81535.1: PID:d1045321: PID:g510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: DNA
A:Residues: 1-235 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNA Res. 6. H3-101. 1999
A:Title: Complete genome sequence of an aerobio hyper-thermsphillic Ciwiarchacon. Actopy A:Reterence number: A*2450; MOID:99310339; PMID:10382966
A:Accession: 372484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Kawarabayasi, Y.: Hino. Y.: Horikawa, H.; Yamazaki, S.; Haikawa, Y.: Jin-no. K.; awa. H.: Takamiya, M.: Masuda, S.: Funabashi, T.: Tanaka, T.: Kudob, Y.: Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aypothetimal protain APE2519 - Aeropyrum pernix (strain El)
C.Species: Aeropyrum pernix
C.Dari- 20-Aug-1999 #seguence_revision 20-Aug-1999 #text_chauge 20-Aug-1999
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A:Accession: $44281
                                                                                                                                              C:Genetics:
                                                                                                                                                                                                                                                                                         A:Status: preliminary
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Cospecies: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Accession: G72484
                                                                                 :Superfamily: mouse l-acylolycerol-3-phosphate O-acyltransferase
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   W. Ltw Lizen
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Local Similarity 100.0%; Pred. No. 93;
Yes 5; Conservative 0: Mismatches
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      100.00
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Scott 25,
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C:Superfamily: mouse 1-acylglyc::21:3 phosphate 0-acyltransferase
C:Keywords: acyltransferase; counzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claycossion: D64688

R:Tomb. J.F.: White. O.: Kerlavano. A.R.: Clayton. R.A.: Sutten. G.G.: Fleischmann.

R:Tomb. J.F.: White. O.: Kerlavano. A.R.: Clayton. F. Khaish. H.G. Slosh-k. A.: M.

Ferterson. G. Tottus. F. Ficher ben. D. Fedson. F. Khaish. H.G.: Rowman. C.: Watth
                                                                                                                                                                                                                                                                                                                                                                                                                            A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUII::1128932: FMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Pate: 20:Apr:2001 *sequence_redision 20:Apr 2001 *text_change 20:Apr:2001 C:Accession: G86920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.D.; Fraser. A:Title: The complete genome sepance of the dastric pathogen Halicohacter pylori. A:Reterence number: A64520; MUID: 97394467; PMID: 9252185
A:Accession: D64688
                                                                                                                                                                                                                              A:Gene: ML0095
                                                                                                                                                                                                                                                            C:Genetics:
                                                                                                                                                                                                                                                                                 A/Cross-references: GB:AL450380; NID:q13092477; PIDN:CAC29603.1; G3PDB:GN00147
                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-302 <STON
                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable integral membrane protein (imported)
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A; Residues: 1-240 < TOM>
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Best Local Similarity lou.
Thos 5; Conservative
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.Date. 09-Aug-1997 #sequence_relision 09-Aug 1997 #text_change 06 Oct-2000
                                                                                                               Matches
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210 LESYT 214
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nes 5; Conser
                                                      1 LESYT 5
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J. Kelley, J.M.: Cotton M.D.: Weldman, J.M.: Pujii, C.: Bowman, C.: Watthey
88, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Rutherford, K.M
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                                                                                                                                    Score 25: DB 2; Fred. No. 1.1e+3;
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Pred. No. 95;
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                                                                                                                                 1.20+02;
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                                                                                                                                                                     Length 302:
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C:Species: Mycobacterium tuberculosis C:Sate: 17 Julily46 #sequence\_te..s.on 17-Julily98 #text\_change 22-Oct-1994

hypothetical protein Rv3806c  $\cdot$  My obacterium tuberculosis (Strain H37RV)

RESULT 12

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conserved bypothetical protein (imported) - Sulfolobus solfatarious
C:Species: Sulfolobus solfatarious
C:Date: 24-May-2001 #sequence_rovision 24-May-2001 #rext_change 15.0un-2001
C:Accession E90199
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A:Molecule type: PMA
A:Residues: 1-133 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2q26040 (imported] - Arabidopsis thaliana N.Alternate names, hypothetical protein T19L18.15 (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001 (c.Baccession: T0261) (G84655 (c.Bacces
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C:Superfumily: conserved hypothetical protein MJ1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
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R.Lin, X.: Kaul, S.: Rounsley, S.D.; Shea, T.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.: Moffat, K.S.; Cronin, L.A.; Shen, M.: VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.: Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMRL Data Library, August 1998
Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence
Reference number: 214681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A:Reference number: A84420: MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-190 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A: Accession: T02619
                                                                                                                         A:Map position: 2
C:Supertamily: Arabidopsis thaliana hypothetical protein T13J8.30
                                                                                                                                                                                                              A; Gene: T19L18.15; At2q26040
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002093; NID:q3413709, FIDN:AAC31232.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-190 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: preliminary
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Accession: E90199
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I.: Jeffries. A.C.: Kozera. C.J.: Medina. N.: Peng. X.: Thi-Ngoc, H.P.: Redder. J.
R.A.: Ragan, M.A.: Sensen, C.W.: Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 LESYT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; toeal Similarity 100.0%;
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        100.0%;
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RISHE, D.: Singh, K.A.: Confabrator, f., Itranschi, Y.: Allard, G.: Awayez, M. Jong, T.: Jeffries, A.C.: Kozena, C.J.: Medina, N.: Peng, X.: Thi Ngoc, H.P.: arrett, R.A.: Ragan, M.A.: Senson, C.W.: Van dei Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Date: 24:May 2001 #sequence_thvision 24:May-2001 #thit_thange 15 Jun 2001 C:Accession: E90187
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C;Supertamily: Methanococcus jaunaschii conserved hypothetical protein MJ0226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Reference number: A99139
A:Accession: E90187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; ramada, Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobarteriu A;Teference number: AB1807; MITT::21595285; PMID::11759840
A;Accession: AH2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type:
A:Residues: 1:19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Kaneko, T.; Nakamura, Y.; Wolk, C.F.; Kuritz, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Nostoc sp. arrain PCC 7:20 is a synonym of Anabaena sp. strain PCC c:pate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_charge 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics
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C:Species: Nostoc so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: GB:AP003602: PIDN:BAB77310.1; PID:q17134752: GSPDB:GN-0181
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                                                                                                                                                                                                                                                                                                                                                                                     A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-215 KUR>
c:Species: Hordeum vulgare (batley)
c:Date: 13-Jan 1995 #sequence_revision 13-Jan-1995 #text_change 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: alr7667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain PCC 7120
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                                                  ES43 protein - barley
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hes 5; Conservation
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S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Taba
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100.0%; Pred. No. 75;
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Copyright (c) 1993 2003 Compagen Etd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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16	25	100.0	ري د د د د د د د د د د د د د د د د د د د	N	F87647	phosphoserine amin
1.7	25	100.0	454	N	T39297	probable atpase -
18	25	100.0	458	₩	E97349	membrane associate
۱4	tu n	104.0	462	N	G01804	interleukin 3-requ
20	25	100.0	470	$\sim$	D41977	retinoid receptor
21	<u>.</u>	100.0	535	N	D71267	probable UDP-N-ace
:5	25	100.0	548	ب1	T16082	hypothetical prote
L.	, n	100.0	597	tu	56761	11
t⊹ 4•	25	100.0	634	N	A25646	dnaK-type molecula
25	t∪ ∵n	100.0	C G G	ŧ.,	A55719	molecu
£5	E.	100.5	749	Ν	B86606	primosomal protein
27	t⊖ Ji	0.001	749	~	G72018	primosomal protein
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E)11-23/momain: signal sequence #status predicted (500 for predicted MAT+E)24-99/Hoduct. Momocyte chemoattractant protein:2 #status predicted MAT+

Query Match

100.0%

Score 25;

DB 2; Length 94

probable thioredo	T08271	,	119	92.0	(4) (1)	. n	
hypothet i	T08158	٠.	117	92.0	23	44	
hypothetic	AG0661	,	112	92.0	23	44 W	
hypothetic	H70141	,	51	92.0	23	42	
polyprotein - fava	T12117	,	5825	100.0	25	41	
tibrillin-	A55624	١,	2871	100.0	25	<b>4</b> 0	
polyket.ide	F69679	٨.	2543	100.0	25	ω Q	
versican precursor	A60979		2409	100.0	ED CD	3 8	
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tMDC II protein .	547656	٠.	756	100.0	25	30	

## ALIGNMENTS

### RESULT 1 JC5295 A:Molecule type: mRNA A:Residues: 1-99 <-H052 A:Residues: 1-99 <-H052 A:Residues: 1-99 <-H052 A:Experimental source: corpus luteum C:Superfamily: macrophage inflammatory protein C:Superfamily: macrophage inflammatory protein C:Superfamily: signal sequence #::atus predicted <SIG> F:1-23/Nomain: signal sequence #::atus predicted <SIG> nonceyte chemoattractant protein 2 precursor pig C:Species: Sus scrofa domestica (domestic pig) C:Species: 24-Feb-1995 \*sequence\_regision 24-Feb-1995 \*text\_change 16-Jul-1999 C:Accession: JC2417 R:Hosang, K.) Knoke, I.; Klaudiny, J.; Wempe, F.; Wattke, W.; Scheit, K.H. R:Josang, K.) Knoke, I.; Klaudiny, J.; Wempe, F.; Wattke, W.; Scheit, K.H. R:Josang, K.) Ges. Commun. 205, 148-153, 1994 A:Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCF-2): AL A:Reference number: JC2417: MUID-75041716; PMID:7999015 A;Gene: mcp-2 C;Superfamily: macrophage inflammatory protein E;1-23/Domain: signal sequence #status predicted <SIG> F;24-49/Fredact, monocyte chemotactic protein-2 #status predicted <MAT-R:Van Coillie, E.; Froyen, G.; Nemiyama, H.; Miura, R.; Fiten, P.; Van Aelst. I.: Van Biochem. Biophys. Res. Commun. 21, 726-730, 1997 A:Title: Human monocyte chemota tic protein-2: cDNA cloning and regulated expression A:Reference number: JC5295; MG1::97224420; PMID::9070881 A:Accession: JC5295 monocyté chemotactic protein 2 (recursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Caccas (2-May-1997 \*Segrence\_: orision 19-7gl-1997 \*Fort\_chango 20-Tun-2000 C;Accassion: JC5295 3 C;Comment: This protein belongs to the beta-chemokine family which is one of the ma tis and in tumor biology, and centribute to the trafficking and recuitment of the re A:Cross-references: GB:Y10802; NID:q1924937; PIDN:CAA71760.1; PID:q1924938 A:Experimental source: bone mar::>>> A; Molecule type: mRNA A; Residues: 1-99 <VAN> RESULT 2 Query Match 100.0%; Best Local Similarity 100.0%; Matches 5; Conservative 0 48 LESYT 52 1 LESYT 5 0: Mismatches Score 25; DB 2; Length 99; Pred. No. 37; 0; Indels Gaps

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sporting table:
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#### RESULT 1 AAY49695 TO AAY4 Harrological decompositive disease HTV-1: envelope protein: gpl20; t.xi; herrological protein: gpl20; t.xi; herrological desth: encyphalepathy: neuropathy: memory loss; demential depression; psychosis; opportunistic intection; neurotoxicity; inflammatory neurological disease; multiple sclerosis; tropical spastic paraparesis; Alzheimer's disease. WPI: 1999-633695/54 FIV 1 qp120 induced neur hal cell death inhibiting peptide #1. 19-JAN-2000 (first entr.) AAY49695 Standard Printil S SOPPAAA Pert C, W09951254-A1. Synthetic. (ADIM-) ADVANCED IMMUNIT :NO 06-APR-1998; 06-APR-1999; 14-0CT-1999 Ruff M; 980S-0080m36. 99W0-US07":4.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome: synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne wulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                       N-PSDB; AAS59578
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU56783 standard; Protein; 50 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides are useful for treating symptoms caused by neuronal cell loss. Such conditions especially associated with HIV infection include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49695 and AAY49696 represent peptides which inhibit HIV-1 gp120
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                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acues
                                                                                                Example 1: SEQ ID No 17978; 1069pp; English
                                                                                                                                   treating acne vulgaris
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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by F. acres. The listaders include SAH, syndime (synchitis, acres, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis
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, Jen S, Carter D;
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Pred. No. 7.8e+05;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acces proteins. These antibodies can be used to downraymate expression and activity of P. acces polypeptides and therefore treat P. acces infections. The antibodies may also be used as diagnostic agents for determining P. acces presence, for example, by enzyme linked immunoscribert assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
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21-SEP-2000; 2000US-0234097
27-SEE-2000; 2000US-0236099
                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 200005-0186 (2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray; Alzheimer's discase; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon: gene expression analysis: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM64554 standard; Protein:
                                                                                                                                                                     WPI; 2001-483446/52
                                                                                                                                                                                                                                                               04-00T-2000; 2000GH-0024263
                                                                                                                                                                                                                                                                                                                         38-78N-2000; 2000MS-0608468
                                                                                                                                                                                                                                                                                                                                         25-MAY-2000; 200008-0207456
                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-USOC667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SE2 ID
                                                                                                                                  Single exem nucleic acts probes for analyzing gene expression in
                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMI : INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LESYT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LESYT 5
                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                    Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25;
Pred. No.
                                                                                                                                                                                                    Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : DB 22;
: 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                      human
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probes which are derived from genomic sequences expressed in the human brain. They can be used to awasure gene expression in brain cell samples which may enable the diametric and improved treatment of nervous system.

such as Altheims's disease

multiple sclerosis, achizophrenia

The present invention provides a number of single exon nucleic acid Example 4; SEQ ID NO:  $\Re E^{RB}$ ; 650pp + Sequence Listing; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                  are useful as medicaments, for diagnosis and/or treatment of diseases which require antagonistic activity of a chemokine e.g. inflammatory diseases. HIV infection, tumours, and anglogenesis, and hematopoicsis related diseases, including auto-immune diseases, atherosclerosis, pulmonary diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a truncated CoC shemoking motocyte observable protein 2 (MCF2) containing amino acids 6.76 of the mature protein. The invention relates the generation of amino-terminal truncated CoC chemokines, having chemokine antagonistic activity. The new chemokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New amino-terminally truncated C-C chemokines have antagonistic activity for treatment of immune, inflammatory and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulated on activation normal T-cell expressed and secreted; RANTES; truncation: antagonist medicaments diagnosis; inflammation; infertion; tumour; andiogenesis, hematropoles.

because in the medicament of the content of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4: Fig 1: 29pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI: 1999 DOTIOS/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISTE ) ARS APPLIED RES SYSTEMS HOLDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY07234 standard; protein; 71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP906954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild type: C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Truncated monocyte chemotactic protein 2 (6-76)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                         tocal Similarity
hes 5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
20 LESYT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 LESYT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LESYT 5
                                                         1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Struyt S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97EP-0116863.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                   100.0%;
                                                                                                                   (2)
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Pred. No. 1.5e+02;
                                                                                                                                                   Score 25; DB 20;
Pred. No. 1 6e+02;
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                            Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                   C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                           This sequence represents a translated C C chemokine monocyte chemotactic protein Z (MCPZ) contained animo acids 6-76 of the mature protein. The invention relates the generation of aminoctorminal crumcated CC chemokines, having chemokine antagonistic activity. The new chemokines are useful as medicaments, for diagonistic activity. The new chemokines and/or treatment of diseases which regular antagonistic activity of a chemokine e.g. inflammatory diseases, HIV infection, fundous, and andiogenesis and hematopolesis—related diseases, including auto-immune diseases, atheroscierosis,
Chemoattractant; MCP-2; h-paranase; heparin; heparan sulfate;
                              Chemoattractant MCP-2.
                                                            29-AUG-1995
                                                                                            AAR70804;
                                                                                                                       AAR70804 standard; Protein;
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                   pulmonary diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1997;
29-SEP-1497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulated on activation resmal T-cell expressed and secreted; RANTES: truncation; antagonist; Redicaments; diagnosis; inflammation; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wild type; C-C chemokine: monocyte chemotactic protein 2: MCP2; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated monocyte chemotactic protein 2 (6-76).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1999 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY07238 standard; protein: 71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity for treatment of immune, inflammatory and infertious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New amino terminally truncated C.C chemokines have antagonistic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 1949-206774/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EF905241-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulmonary disease; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour; anglogenesis; hematopolesis; autoimmune disease; atherosolerosis,
                                                                                                                                                                                                20 LESYT 24
                                                                                                                                                                                                                            1 LESYT 5
                                                                                                                                                                                                                                                          Conservative
                                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97EP-0116863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97EP-0122471
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                                                                                                                                                                                                                                                                         100.
                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                       Score 25; DB 20;
Fred. No. 1.6e+02;
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                     Length 71;
                                                                                                                                                                                                                                                          Indels
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AAY69031
ID AAY
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening for cpds, with anti-heparanase activity - by detecting inhibition of heparin or heparan sulphate degradation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1993;
13-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis: restenosis; cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in ARR70786-804. Most are prepared by reverse transcription of mPNA from activated human leukocytes, then clouing of the cDNA into pVL1392 baculovirus vector, and expression in Sf9 cells in the presence of reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 53; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potentially useful for treating arthritis, restenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 1995-082239/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hooywert AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UPJO ) UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                  AAY69331 standard; protein; 76 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutathione and dithiothreitol.
                                                                                      03-EEB-2000
                                                                                                                                                                                                      secondary tissue damage; central nervous system injury; MCP-2; CNS inflammatory disease; neurodegenerative disorder; heart disease; inflammatory bowel disease;
                                                                                                                                                                                                                                             Chemokine receptor; ligand; inflammatory response; immune effector cell;
                                                                                                                                         Homo sapiens.
                                                                                                                                                                 inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer
                                                                                                                                                                                                                                                                      Amino acid sequence of chemokine receptor ligand MCP-2.
                                                                                                                                                                                                                                                                                                 30-MAY-2000 (first entry)
            (OSPR-) OSPREY PHARM LTD
                                                              21-JUL-1999;
                                                                                                                                                                                            inflammatory
                                      22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   23 LESYT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ledbetter SR;
                                                                                                                                                                               joint disease; inflammatory kidney; renal disease; lung disease; inflammatory masal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0136117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99866001-Sut 6
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                                       98ns-0120523
                                                               99WO-CAOO659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 16;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
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The present sequence represents a chemokine receptor ligand. The present of ingand can be incorporated into the conjugates of the invention. The conjugate comprising a targeted agent and a confident of the conjugate binds to a chemokine receptor ligand. The conjugate binds to a chemokine receptor receptor. The conjugates are used for formulating a medicament or for contracting in internalisation of the targeted agent in cells bearing the receptor. The conjugates are used for formulating a medicament or for contracting disorders associated with inflammatory responses resulting from contraction, proliferation and migration of immune effector cells. The conjugates states comprise secondary tissue damage such as contral nervous system (CMS) injury. CMS inflammatory diseases, inflammatory bowel diseases, inflammatory joint diseases, inflammatory by the inflammatory or renal diseases, inflammatory lung diseases, inflammatory consall diseases, inflammatory thyroid diseases, inflammatory and diseases, inflammatory lung diseases, inflammatory consall diseases, inflammatory thyroid diseases such as thyroiditis, or contraction contractions and contractions are diseases.
                                                                                                                                                                                                                                                                                           Ş.
                                                                                                                                                                                                                                                  P
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Thomas 5; Conserv
                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new therapeutic agent comprising a conjugate for treating secondary tissue damage and other disease conditions like Alzheimer's disease stroke, Parkinson's disease and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McDonald JR, Coggins PJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure: Page 60; 204pg. English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytokine-regulated cancers
                                                                                                                                      AAO21099 standard: Protein.
protein of WT-MCP-2
                                           19-JUL-2002 (first entr)
                                                                                        AA021099
                                                                                                                                                                               œ
                                                                                                                                                                                                                                                  25 LESYT 29
                                                                                                                                                                                                                                                                                                1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                        76 AA;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                   Score 25.
Pred. No.
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                          DB 21;
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                         Indels
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A mutant of the human CC chemokine RANTES with two mutations in the callionic site of the 40 ^{\prime}\mathrm{C} loop is used for treatment of multiple sclerosis and/or demyelizating diseases -
                                                                 WPI; 2002-340073/37
                                                                                                           (ISTF ) ARS APPLIED RES SYSTEMS HOLDING
                                                                                                                                   04-OCT-2000; 2000EP-0121555
                                                                                                                                                          03-OCT-2001; 2001WO-EP11428
                                                                                                                                                                                11-APR-2002
                                                                                                                                                                                                        WO200228419-A2
                                                                                                                                                                                                                                                inflammatory disease; demyelinating disease; allergic
Examples: Page 46: 46pp; English
                                                                                       Proudfoot A, Wells INC,
                                                                                          Kosco-Vilbois
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PANTES: neuroprotective: antiallergic: antiinflammatory anti-HIV: chemokine mutant; cattonic site; multiple sclerosis; HIV infection:

anti-HIV; human;

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AAO21109
DЬ
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                             demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents an example of a co
                                                                          The invention relates to a truncated and mutated human RANTES (a CC chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other
                                                                                                                                                                                                                     A mutant of the human CC chemokine RANTES with two mutations in the cationic site of the 40's loop is used for treatment of multiple sclerosis and/or demyelinating diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a truncated and mutated human RANTES (a CC chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents an example of a wild-type
                                                                                                                                                                                      Disclosure; Fig 1; 46pp; English.
            chemokine protein
                                                                                                                                                                                                                                                                                                                                    Proudfoot A, Wells INC,
                                                                                                                                                                                                                                                                                                                                                                  (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV
                                                                                                                                                                                                                                                                                                                                                                                                    04-001-2000; 2000EP-0121665
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-UCT-2001; 2001WO-EP11428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W0200228419-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANTES: neuroprotective; antiallergic; antiinflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA021109 standard; Protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disease; demyelinating disease; allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCP-2 chemokine protein containing 40's loop and cationic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemokine protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= 40's_loop
46..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Cationic_site
          operaining a 40's loop and opening site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                   Kosco-Vilbois M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 23; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                   here the antigen present is the composition is a tumour associated antigen. The use of APC claimotaxins provides an accelerated immune response in a bast following administration of antigen, a more effective temponse to administratification, in exposure to, very small quantities of
                                                                                             infectious pathmyrnic agents (bacteria, virus, etc.,) prior to expected or possible exposure, for treating cancers, melanomas, throughout carcinomas, lung and breast cancers, renal cell carcinomas etc.
                                                                                                                                                                              separately. Synthetic (mimetic) or naturally occurring chemokines may be used. The polypeptides of the invention are used to induce an immune response by recruiting AFEs to areas of antigen contact. The compositions
an antigen (e.g., toxin () pathogen) due to increased autigen uptake
                                                                                                                                                                                                                                                                                                      subject, in the manufacture of a medicament, where the APC-chemotaxin is a chemokine polypeptide or its variant, or a polynocleotide encoding the chemokine polypeptide or its variant. The invention has antitumour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of a composition containing an antigen presenting cell-chemotaxin which is a chemokine polyreptide or its variant or a polynucleotide encoding the protein, for inducing immune response to an antigen in a
                                                                                                                                                                                                                                            and may be administered in the same mixture as the APC chemotaxin or
                                                                                                                                                                                                                                                               Can contain and antimicrelial activity. The compositions of the invention can contain one or more ortigens (or antigen containing polynucleotides)
                                                                                                                                                                                                                                                                                                                                                               describes the use of a composition containing an antigen presenting cell (APC) -chemotaxin for inducting an inmune response to an untigen in a
                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a human chemokine polypeptide designated hMCP-2, used in the compactions of the invention. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-034405/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schall TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHEM-) CHEMOCENTRYX INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokine; antitumour; cytostatic; antimicrobial; toxin; pathogenic agent; cancer. melanoma; thyroid carcinoma; hMCP-2. renal cell carcinoma; tumpur-associated antigen; human; hMCP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human chemokine hMCP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG78390 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen presenting cell; APC; chemotaxin; immune response; antigen;
                                                                                                                                                             the invention are useful for providing protection from foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 LESYT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 0%; Score 25;
100 0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 11
AAG68353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pb
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                                                                                                  The present invention describes a method for inducing an immune response to an antigen in a subject. The method comprises administering a composition containing an antigen presenting real chemotaxin of composition containing an antigen-presenting real chemotaxin and containing an antigen-presenting real chemotaxin of composition containing an antigen-presenting and chemotaxin by appendix of its variant. The AFC-chemotaxin has cytostatic, antimicrobial and containing the activities, and can be used in variant production. The method can be used for inducing or enhancing an immune response, or or for providing protection from exogenous foreign infectious pathogenic or for providing protection from exogenous foreign infectious pathogenic capents prior to expected or possible exposure, or to individuals capents prior to expected or possible exposure, or to individuals capents prior to expected or possible exposure, and tumours. C. c. breast cancer, lung cancer, carcinomas, melanomas, and tumours. C. the present sequence represents a human monocyte chemotactic protein 2 present invariance and sequence, which is used in an example from the corresponding and protein a protein and contains and contains a contains and contains a contains and contains a contains a contains and contains a contains a contains a contains a contains and contains a contains 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Matches
                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human: mouse: monocyte chemotactic protein 2; hMCP2; MCP2; MCP0; chimeric chemokine: immune response; cytostatle; antimicrobial; immunostimulant; vaccine; cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human monocyte chemotactic protein 2 (MCP2) amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma, melanoma; tumour; hybrikine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing an immune response to an antigen to confer non-specific protection while the body is generating the adaptive response comprises administering a composition containing an antigen-presenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200180887-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000: 2000US-198839P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-2001; 2001W0-US12162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHEM-) CHEMOCENTRYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Fig 2; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell chemotaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 LESYT 29
                                                                                                                                                 present invention for the design of hybrikines (chimeric chemokines).
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LESYI 5
  Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Talbot D;
  Conservative
                              100.0%; Score 25; DB 23; 100.0%; Pred. No. 1.7e+02;
          0;
          Mismatches
                                                            DB 23; Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 76;
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                        Gaps
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26 LESYT 30

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RESULT 12
AAB15786
ID AAB15
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                                 Best Local Similarity
Matches 5; Conserv
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoryte chemoattractant protein-1; inflammation; atherosclerosis; HIV: monoryte chemoattractant protein-1; inflammation; atherosclerosis; HIV: AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia; basophil-mediated disease; myocardial infarction; acute ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human chemokine MCP-2 SEQ 1D NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB15786 standard; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1999;
17-MAR-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macrophage recruitment; chamokine derivative; MCP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB15786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 47
                                                                                                                                             The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, agonists and achemokines which are then useful in disease treatment. The chemokines antagonists which are then useful in disease treatment. The chemokines antagonists which are then useful in disease treatment. The chemokines can be used to treat diseases such as these can be used to treat diseases such as autommune diseases, atheroscierosis, osteoporosis, HIV inherition and autommune diseases, atheroscierosis, osteoporosis, HIV inherition and AIRS, psoriasis, inflammatory diseases, hypertension, hasophil-mediated AIRS, psoriasis, inflammatory diseases, hypertension, hasophil-mediated diseases, endotroxemia, myocardial infarction, acute incharmia and diseases, endotroxemia, myocardial infarction, cute incharmia and remumatoria architis, and can be used to prevent strokes and as remained therapy for the same diseases, as well as in the production of gene therapy for the same diseases, as well as in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; contraception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200042071-A2
                                                                                                                                                                                                                                                                                                                                                                                                        New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vaccular diseases, autoimmune diseases and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grainger DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA74886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-2000; 2000W0-HS00821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 LESYT 29
                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 134; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     treating e.g. stroke,
                                                                                                 Sequence
                                                                                                                                    animal models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LESYT 5
1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-499101/44.
                                                                                                        77 AA;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0229071.
99US-0271172.
99US-0452476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tatalick LM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "en oded by CAA"
                                                   0;
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                                          Mismatches
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AAG78395
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                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                        CC The invention relates to polynucleutides encoding murine, Julies Fig. CC human ectaxin polypeptides. The ectaxin polynucleotides are useful for commodulating ensinophil chemotaxis, for increasing ensimphil chemotaxis, for increasing ensimphil chemotaxis, for increasing ensimphil chemotaxis, for increasing ensimphil chemotaxis, for increasing ensimphilis of the events, and for improving prognosis with tumourigenesis, and for calso useful for treating inflammation and tumourigenesis, and for ceducing inflammation and cytotoxic damage caused by ecsinophils, for e.g. during asthmatic reactions, essimphilis pneumonia and allorgic constitutis, parasitic infections and ecsimphili cardiac diseases. The vasculitis, parasitic infections and ecsimphili cardiac diseases. The constitution polynucleotides are also useful for modulating histamine release by modulating estaxin activity or expression during anaphylaxis, curticaria and altergic reactions. They are useful for detecting and continuing ecsimphil mediating conditions, and in anti-cancer gene curtoring essingbil mediating conditions, and monocyte chemoatitiactive protein (MCP) 2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
ABB80903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
AAG78395;
                             AAG78395 standard; protein; 77 AA
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disciosure; Fig 3B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA encoding murine, guinea pig or human eotaxin polypeptides, useful for treating inflammation and tumorigenesis and in anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 2002-565447,760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eotaxin; eosinophii; chemotaxis; cytostatic; antiinflammatory; cardiant; antiallergic; immunosuppressive; antiasthmatic; antiparasitic; histamine; dermatological; vasotropic; monocyte chemoattractive protein; MCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luster AD, Leder P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE (GEHO ) GEN HOSPITAL COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-sep-lees;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6403782-BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; antianaphylactic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-00T-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80903 standard: Protein; 77 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 - mn-1995 -
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                                                                                                                           11111
25 LESYT 30
                                                                                                                                                                                                    Local Similarity
nes 5; Conserv
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                                                                                                                                                                                                                                                                            77 AA;
                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9505-0522713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0366887.
                                                                                                                                                                                                                 100.0%; Score 25; DB 23; 100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothenberg M, Garcia E;
                                                                                                                                                                                                  0;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                 Length 77,
                                                                                                                                                                                                  Indels
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                                                                                                                                                                                              Gaps
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(bacteria, virus, etc.,) prior to expected or possible exposure; for treating cancers, melanomas, thyroid carcinomas, lung and breast cancers, renal cell carcinomas etc., here the antigen present in the composition is a tumour-associated antigen. The use of Apc-chemotaxins provides an accelerated immune response in a host following administration of antigen, a more effective response to administration of or exposure to very small quantities of au antigen (e.g., toxin or pathogen) due to increased antigen uptake by APCs, and more effective anti-tumour
                                                                                                                                                                                                                                     antigen containing polynumleotides) and may be administered in the same mixture as the APC-chemotaxin or separately. Synthetic (minetic) or naturally occurring chemokines may be used. The polypetides of the invention are used to induce an immune response by recruiting APCs to areas of antigen contact. The compositions of the invention are useful for providing protection from foreign infectious pathogenic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a chimeric chemokine polypeptide (bybrikkine) derived from tunnan chemokine hMCF 2 (AAC78390) and murine chemokine mMDC (AAG78392) used in the compositions of the invention. The specification describes the use of a composition containing an antigen presenting cell (APC)-chemotaxin for inducing an immune response to an antigen in a subject, in the manufacture of a medicament, where the APC-chemotaxin is a chemokine polypeptide or its variant, or a approximation is a chemokine polypeptide or its variant, or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of a composition containing an antigen presenting cell-chemotaxin which is a chemokine polymeptide or its variant or a polymecleotide encoding the protein, for inducing immune response to an autique in a
                                                                                                                                                                                                                                                                                                                                                                         compositions of the invention can contain one or more antigens (or
                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide encoding the chemokine polypeptide or its variant. The invention has antitumous cytostatic and antimicrobial activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 2, 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-034405/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-1988 (P. 12-APR-2001; 2001US-0834H14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen presenting cell; APC; chemotaxin; immune response; antigen; chemokine, antitumour; cytostatic; antimicrobial; toxir; pathogenic agent: cancer melanoma; thyroid carcinoma; hybridkine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APP 2001; 2001W0-8812980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0100180882-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHEM-) CHEMOCENTRYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse/human hybridkine mMNC/hMCP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              renal cell carcinoma; tumour-associated antigen; human; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note+ "Grresponds to residues 1:13 of mMHC (AAG78392)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Corresponds to residues 11-76 of hmdp2 (AAG78390)"
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Best Local Similarity

100.00;

Score 25; Fred. No.

DB 23;

Length 77,

Sequence

77

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RESULT 15
AAG68358
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                                                                                                                                                                                    The present invention describes a method for inducing an immune response to an antigen in a subject. The method comprises administering a composition containing an antigen-presenting cell chemotaxin composition containing an antigen-presenting cell chemotaxin according to the chemotaxin, where the APC-chemotaxin is a chemokine polypeptide, are interested in a polypeptide or contained to a polypeptide encoding the chemokine polypeptide or content and can be used for inducing an encoded in a production. The method can be used for inducing or enhancing an immune response, confort providing protection from exogenous foreign infectious pathogenic confort providing protection from exogenous foreign infectious pathogenic conforts prior to expected or possible exposure, or to individuals confort to expected or possible exposure, or to individuals confort to expected or possible exposure, or to individuals confort to expected or constant and the method may be used to treat cancers confort to expected or constant and the present cancers to the present sequence represents an exemplary chimeric chemokine from the present of invention for the design of hybrikings (chimeric chemokines).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                     Query Match
Best Local Similarity
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mouse; monocyte chemotactic protein 2; hMCP2; MCP2; mCP0; mMPC; chimeric chemokine; immune response; cytostatic; antimicrobial; immunostimulant; vaccine; cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric chemokine mMDC/hMCP2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma; melanoma; tumour; hybrikine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing an immune response to an antigen to confer non-specific protection while the body is generating the adaptive response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schall TJ. Talbot D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHEM-) CHEMOCENTRYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AFR-1000; 2000US-198839F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 2002-049246/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell chemotaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises administering a composition containing an antigen-presenting
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 LESYT 30
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26 LESYT 30
                                  1 LESYT 5
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                                                                                                                                                   77 AA;
                                                                         Conservative
                                                                                            100.0%;
100.0%;
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                                                                                              Score 25; DB 23;
Pred. No. 1.7e+02;
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                                                                           Mismatches
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                                                                                                                Length 77;
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                                                                                   Gaps
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Search completed: April 8, 20(3, 12:01:37 Job time : 45.3333 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and is derived by analysis of the total score distribution
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1: /cgn2_6/ptodata/1
2: /cyn2_6/ptodata/1
3: /cyn2_6/ptodata/1
4: /cyn2_6/ptodata/1
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Match
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/cgn2_6/ptodata/1/laa/5A_COMB.pep.*
/cyn2_6/ptodata/1/laa/5A_COMB.pep.*
/th2_6/ptodata/1/laa/6A_COMB.pep.*
/th2_6/ptodata/1/laa/FTTUS_COMB.pep.*
/gn2_6/ptodata/1/laa/FTTUS_COMB.pep.*
                                                    US-09-562-737-116
US-09-181-562-4
US-09-131-4001C-3736
US-09-134-664-20
US-08-436-664-32
US-08-436-664-32
US-08-135-642-32
US-09-135-642-32
US-08-134-22A-32
US-08-394-322A-34
US-08-394-322A-34
US-08-394-322A-34
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US-DH 48D-449-20

US-DB-66D-542-20

US-DB-47D-603-20

US-DB-47D-603-20

US-DB-43D-144A-6

US-DB-34D-144A-6

US-DB-36D-887A-112
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US-08-951-871-6
US-09-134-0010-4633
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⊕S+08+470+323+6
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                                                                                                                                                          Sequence 6, Appli
Sequence 4644, Ap
Patent WI. 5180808
Sequence 115, Appli
Sequence 4, Appli
Sequence 3736, Ap
Sequence 20. Appl
Sequence 31. Appl
Sequence 31. Appl
Sequence 32. Appl
Sequence 33. Appl
Sequence 30. Appl
Sequence 31. Appl
Sequence 32. Appl
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Sequence 20, Aggl
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ecuentaes
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Sequence 488, App
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Section   Sect	45	44	<b>\$</b>	40	<b>*•</b>	40	ž	38	3.7	36	3. Un	34	e a Car	w ₹3	31	U.S.	ij	C4 OC:
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Compose   Comp	88.0	88.0		ं अख	0.88		8.0	ુ. ઝલ			88.C						¥.	92.0
7.1679 - 0.1790 - 2.1	120	87	ch.	6.9	68	(A Ca)	n J	:5	1.	1	1.	14 04	-	11	954	(E - J) (T	, ¢,	976
7.1679 - 0.1790 - 2.1	43-	4.	ı.n	ته.	٠,	1,91	••	<b>_</b>			ŧ.		_	_	C.	ÇF	7	,n
	US-08-890-865A-13	US-09-376-330-35	PCT-US96-08295-10	US-09-460-505-10	UC+08+588+258B+10	5332669-2		181.80	-08-179-	-09-347-504	.08 245 151	-08-406-192-	-08-456-424	US-08-456-424-2	US-09-057-969-2	PCT-US95-04080-34	PCT-US94-04090-32	PCT-US95-04080-20
2.0 Appl Appl Appl Appl Appl Appl Appl Appl	Sequence 13,	Sequence 35,	Sequence 10,	Sequence 10,	Sequence 10,	un	1.3		9		Sequence 2,	Sequence 2,	<u>.</u>	ы	Ŋ	Sequence 34,	Sequence 32.	Sequence 20,

## ALIGNMENTS

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TYPE, amino accid
STRANDECHESS, single
TOPCIOSY, linear
MOLECULE TYPE: peptide
US-09-615-232A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/98615232A Patent No. 5993814 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      FILING DATE: TH 94 NOWLE APPLICATION NUMBER: TH 94 NOWLE FILING EATE: 29-APR-1994 ATTORNEY, AGENT INGCEMAT: H: NAME: WILSON, MARY J. NAME: WILSON, MARY J. 12,955
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE. 13-AUG-1996
CLASSIFICATION: 424
FRICE APPLICATION DATA:
APPLICATION NUMBER. 99318
FILING DATE: 14-SEP-1993
APPLICATION NUMBER.
                                                                                                                                                                                               TELEPHONE: (703) 816-40 TELEFAX: (703) 816-4100 INFORMATION FOR SEC ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
AFFLICATION FALLOASE #1.0, Version #1.25 (EPC)
CURKENT AFFLICATION BALLOASE #1.0, Version #1.25 (EPC)
AFFLICATION NUMBER: PATE 10.00 (15.232A)
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH, 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WILLIAMS, T.MOTHY J.
APPLICANT: GOSE, PETER J.
APPLICANT: GRIFFITHS-J-BNSON, DAVID A.
APPLICANT: HEMAN, JOHN J.
TILLE OF INVENTION. GB MCTATITE CYTEK!
NUMBER OF SEQUENCES. 11
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                                                                                                                                        TYPE. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 NOR CITY: ARLINGTON STATE: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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1100 NORTH G'EBE ROAD, STH FLOOR
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                                                                                                                                                                                                                                         (703) 816 4000
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Score 25;
Pred. No.
                     Length 74;
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; ORGANISM: human
US-08-470-323-6
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: LENGIH: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20. Application US/08480449 Patent No. 5688927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER 33,03,43,43,333A CURRENT FILING DATE: 1995-06-06 EARLIER APPLICATION NUMBER: PCT/3894/02006 EARLIER FILING DATE: 1994-09-14 EARLIER APPLICATION NUMBER: GB 9318984.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHEMOTACTIC CYTOKINE FILE REFERENCE: 550-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WILLIAMS, TIMOTHY J. APPLICANT: JOSE, PETER J. APPLICANT: GRIFFITHS JOHNSON, DAVID A. APPLICANT: HSUAN, JOHN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DUS/MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godiska, Ronald APPLICANT: Gray, Patrick W. TITLE OF INVENTION: MACROPH
NAME: Gass, David A.
REGISTRATION NUMBER: 38.153
REFERENCE, COTKET NUMBER 278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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CITY: Chicago
                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                 FILING DATE: 530
                                                                                                                                                       APPLICATION NUMBER: US/08/480,449
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                                                                                                                                                                                                                                                                                            60606-6402
                                                                                                                                                                                                                                                                                                           Illinois
United States of America
                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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RESULT 4
US-08-716-188-3
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                                                                          US-08-716-188-3
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Patent No. 5908829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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Query Match 100 0%, Score 25, DB Best Local Similarity 100.0%; Pred. No. 41; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                APPLIANCE APPLIANCE APPLIANCE APPLICATION: 530
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: FOI/356
APPLICATION NUMBER: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: KELLY,
                                                                                                                                                                                            TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF TITLE OF INVENTION: THE CERVIX NUMBER OF SEQUENCES: 7
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TTTX: 25-3856
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4(91
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GR 9406463.1 FILING DATE: 31-MAR-1-994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHERENT APPLICATION DATA.

APPLICATION NUMBER: U.
                                                                                          MOLECULE TYPE: peptide
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OTHER INFORMATION: "Hu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C
STREET: 1100 NORTH GLESE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LESYT 5
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                     NAME: SADOFF, B.J. REGISTRATION NUMBER:
                                                                                                           TOPOLOGY:
                                                                                                                          STRANDEDNESS:
                                                                                                                                              TYPE:
                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                           Linear
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100 0%; Pied. No. 41;
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                                        DB 2; Length 76;
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           Indels
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1 LESYT 5

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US-08-479-603-20
                                                                                             RESULT 6
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             Sequence 20. Applicat
Patent No. 6320023
GENERAL INFORMATION:
                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER - 08/47
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Godiska, Konaru
APPLICANT: Gray, Patrick W.
FITLE OF INVENTION: MACPOPHAGE DEPIVED CHEMOKINE AND CHEMOKINE
TITLE OF INVENTION: ANALOGS
TITLE OF INVENTION: ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660.542
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STREET: v.
STREET: Thicago
CITY: Thicago
TMATE: Illinois
TMATE: Thited
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/EVOCKET NUMBER 27 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                            Match 100.0%; Score 25; DB Local Similarity 100.0%; Pred. No. 41; hes 5; Conservative 0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/59
FILING DATE: 16-NOV-1995
                                                                                                                                                     25 LESYT 29
                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                         1 LESYT 5
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60606-6402
                                                     Application HS/08479603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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312/474-0448
Godiska, Ronald
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OTHER INFORMATION:
US-08-479-603-20
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/CR347492B Patent No. 5602008
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                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                         APPLICANT: Hawkins, Philt: P.
APPLICANT: Bendman, Olga
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES,
TITLE OF INVENTION: PROTOTION AND USES
NUMBER OF SEQUENCES: 12
SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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DEBATING SYSTEM. FG (AC)MS-DOS

SOFTWARE: PALENTIA REVASE #1.0, Version #1.25

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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TITLE OF INVENTION: MACH PHAGE DERIVED CHEMOKINE NUMBER OF SEQUENCES: 24
                                                                                                                                                             STREET: 3174 Por CITY: Palo Alto
                                  OPERATING SYSTEM:
                                                        COMPUTER:
                                                                                                                              COUNTRY:
                                                                                                                                                   STATE:
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STRANDEDNESS: sir
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CLASSIFICATION:
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COMPUTER: I
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STATE: Illino
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                                                                                                              94304
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60606-6402
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                                                                                                                              U.S.
                                                                                                                                                                                                                                                                                                                                                          Wilde, Craig
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                                              IBM Compatible
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                                                                                                                                                                                                      Incyte Pharmaceuticals, Inc
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Matches 5: Conserv
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PRICE APPLICATION DATA: 98-/2013
APPLICATION NUMBER: 98-/2013
APPLING DATE: 97-SEP-100
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TELEDOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE: Peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLOVE. GI 126829
8-447-4928-9
                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INVENTION. NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRESPONDENCE ADDRESS:
         SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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STREET: 3174 Forter Drive
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                                                                                                                                REGISTRATION NUMBER: 339
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                      FILING DATE:
                                                                              TELEFAX:
                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                      APPLICATION NUMBER. US/08/421,144A
STRANDEDNESS:
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05-007-1994
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single
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100.0%; Fred. No. 42;
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 Mismatches

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: MOLECULE TYPE: protein US-08-421-144A-6
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                                                                                                                                                                                                US-08-798-143-9
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Best Local Similarity 100. 8: Pred. No. 42:
Matches 5. Conservative (): Mismatches
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APPLICANT: Wilde, Craig
                                                              Best Local Similarity Matches 5; Conserv
                                                                                                                                 Query Match
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INFORMATION FOR SEQ ID NO.
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jettrey
APPLICANT: Seilhamer Volumer (Property of the Property of the 
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CORRESPONDENCE ADDRESS: 12
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-NOV-
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TELEPHONE: 415-855-05%
TELEFAX: 415-852-019
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AITOKNEY/AGENT INFORMATI :N:
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LIBRARY: GENBA
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/303.241 FILING DATE: 07-SEP-1994 APPLICATION NUMBER: 09/320.011
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                                                                                                                                                                                                                                      CLONE: GI 126829
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   1 LESYT 5
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                                                10: 0%; Score 25; DB
nilarity 10: 0%; Pred. No. 42;
Conservativ: 0; Mismot-1
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26 LESYT

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APPLICANT: LEDER, PHILIP
APPLICANT: GARGIA, EDUARDO
TITLE OF INVENTION: ECTAXIN: AN ECSINOFHIL CHEMCATTRACTANT
FILE PETERNCE: 00183/025002
CURRENT APPLICATION NUMBER: (85/04/%», %87A
CURRENT ELLING DATE: 1999-08-04
PRIOR FILING DATE: 1995-06-04
PRIOR FILING DATE: 1995-06-22
PRIOR FILING DATE: 1995-06-22
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEC IC NOS. 27
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: ORGANISM: Homo sapions
US-09-366-987A-12
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US-09-227-357-499
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APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 489. Application TS/09227357 Patent No. 6342581
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Best Local Similarity 100.0%, I
Matches 5 Conservative 0.
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SEQ ID NO 12
LENGIH: 77
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EARLIER APPLICATION NUMBER: 60/051,916 EARLIER FILING DATE: 1997-07-08 EARLIER APPLICATION NUMBER: 60/051,940 EARLIER FILING DATE: 1997-07-08 EARLIER APPLICATION NUMBER: 60/051,918 EARLIER FILING DATE: 1997-07-08
                                                                                                                                           EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
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EARLIER APPLICATION NUMBER: 60/052,732
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                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/051,925 EARLIER FILING DATE: 1997-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1998-07-07 EARLIER APPLICATION NUMBER: 60/051,926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE:
                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/051,931
                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/052,803
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US-08-951-871-6
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; Patent No. 5866398
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Best Loral (
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: XT, SHUANG-YONG
APPLICANT: XTAO, JIAN-PING
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EARLIER FILING DATE: 1997-09-12
EAPLIER APPLICATION NUMBER 6070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1997-08-18
EARLIER AFPLICATION NUMBER 60/0
EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
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EARLIER FILING DATE: 1997-08-18
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WARLIER FILING DATE: 1997-07-08
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EARLIER APPLICATION NUMBER:
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NUMBER OF SEQ ID NOS: 672
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EARLIER FILING DATE: 1997-68-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 255
                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                   COFFESPONDENCE ADDRESS:
                                                           NUMBER OF SECUENCES.
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                   ADDRESSEE:
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APPLICATION NUMBER: 60/0
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E: New England Biolabs, Inc
32 Tozer Road
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                                                                                                   METHOD FOR CLONING AND PRODUCTION THE HELL RESTRICTION ENDONUCLEASE IN E.
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RESULT 13
US-09-134-001C-4633
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                                                                                                                                                                              US-09-134-001C-4633
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION HUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064-964
PRIOR FILING DATE: 1997-10-8
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 463s, Application 05/091340010 patent No. 6380370
                                                                                                                                                                                                                                          SEQ ID NO 4633
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 25: DB 2: Length 301; Best Local Similarity 100.0%; Pred. No. 1.7e+02, Matches 5: Conservative 0; Mismatches 9; Indels
                                                                                                                               Query Match
                                                                                     Matches
                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 978-927-5054
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291 LESYT 295
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
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                                                                                                          100.0%; Score 25; DB 4: 100.0%; Pred. No. 3e+02;
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                                                                                          Mismatches
                                                                                                                                      DB 4; Length 538;
                                                                                          0;
                                                                                            0;
                                                                                            Gaps
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PACENT NO. 5180808

PATENT NO. 5180808

FOR TITLE OF INVENTION: VERSI-AN CORE PROTEIN, NUCLEIC ACID

SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROSES, ANTI-VERSICAN

ANTIBODIES, AND METHODS OF DETECTING THE SAME

NUMBER OF SEQUENCES: 4

NUMBER OF SEQUENCES: 4
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Best Local Similarity
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US-09-562-737-116
Search completed: April- 8. . . . . . 12:05:51 Job time : 16.4167 secs
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APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Faceptor Signaling Fathways
FILE REFERENCE: UTSW0708
CORRENT AFFLICATION NUMBER: 18,79,562,737
CUPPENT FILING DATE: 2000 05-01
NUMBER OF SEQ ID NOS: 13,700
NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic other information: Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Local Similarity 80.(%)
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tive 0; Mismatches 0;
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Pred. No. 3e+02;
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                  Pref N is the buffer of results predicted by classe to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10 0 ,
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           9 US-09-792-793A-11
9 US-09-427-444A-14
9 US-01-920-137A-10
10 US-02-920-137A-10
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08-09-195-457-6
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Sequence 11, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 201, Appl
Sequence 201, Appl
Sequence 404, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
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Sequence 17, Appl
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0.8-10-150-501-14 0.08-03-43-130-61 0.08-03-25-400-1170 0.08-03-38-626-5367 0.08-03-88-216-4

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GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS JOHNSON, D.
APPLICANT: HSUAN, JOHN J.
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; Patent No. US20020081623A1
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US-09-792-793A-21
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: AA357020.1, EVALUE 1.00e-07
3-09-864-761-46020
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46020
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LENGTH: 74
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                                    GENERAL INFORMATION:
                                                        Sequence 21, Application US/09792793A Patent No. US20020168370Al
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PRIOR APPLICATION NUMBER: US 09/608.408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/214,687
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CURPENT FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/470,323
PRIOR FILING DATE: 1995-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1' NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
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APPLICANT: Coggins, Philip
                   APPLICANT: McDonald, John R.
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 LESYT 29
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                                                                                                                                                                                                                                                                                     Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                    23 LESYT 27
                                                                                                                                                                                                                         1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRIFFITHS - JOHNSON, DAVID A.
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                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pred. No. 34;
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                                                                                                                                                                                                                                                                                          Score 25; DB
Pred. No. 37;
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                                                                                                                                                                                                                                                                                                               DB 10; Length 74;
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US-08-927-939-17; Sequence 17, Application US, 8927939; Patent No. US20010006640A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo saplens
US-08-927-939-17
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                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-057-275-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 17
LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                               Patent No. US20020155545Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10057275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Compounds and methods to inhibit of IIILE OF INVENTION: augment an inflammatory response. FILE REFERENCE: 295.022081
CURKENT APPLICATION HUMBER: 08/08/027.939
CURRENT FILING DATE: 1997-0-11
NUMBER OF SEQ. ID NOS: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 5, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Çmery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Grainger, David 1.
APPLICANT: Tatalick, Lauen Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE, fastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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nes 5; Conserv
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               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                     NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCKEAS
                                                                                                                                                                                                                                                                   APPLICANT: Coleman, Roger
                                                                       COUNTRY: U.S.
                                                                                             STATE: CA
                                                                                                                               STREET: 3174 Porter Drive
COMPUTER: IBM Compatible
                                                                                                             CITY: Palo Alte
                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc
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                                                                                                                                                                                                                                 Wilde, Craig G
                                                                                                                                                                                                                                               Bandman,
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Fred. No. 38;
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OPERATING SYSTEM: DOS

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RESULT 7
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: ORGANISM: Homo sapiens
US-09-834-794A-24
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                                                                                                                                                                                                                                        SEQ ID NO 24
LENGTH: 77
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                                                                                                                Matches
                                                                                                                                                 Query Matich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/04434794A Publication No. US20030026777A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/146,580 PRIOR FILING DATE: 1998-09-03 PRIOR APPLICATION NUMBER: 60/071,899 PRIOR FILING DATE: 1998-01-20 PRIOR APPLICATION NUMBER: 60/092,155 PRIOR FILING DATE: 1998-07-09
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                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/04/44 794A CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lawrence, Papsidero APPLICANT: Lyn, Dyster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Detection and Treatment of Breast Cancer FILE REFERENCE: 3380/11127\text{-}US4
                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFURMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                              26 LESYT 3
                                                                                                                        Match 100.0% Score 25; EB Local Similarity 100.0%; Pred. No. 39;
                                                                                  1 LESYT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/POCKET NUMBER: FF-3027 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
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APPLICATION NUMBER: US/10/U57,275
FILING DATE: 25-Jan-2002
PRIOR APPLICATION DATA:
                                                                                                                  S,
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TYPE: amino acid
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyn, Dyster
Jana, Frustaci
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CLONE: MCP-2
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                                                                                                                  Conservative
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Pred, No. 39;
                                                                                                             Mismatches
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                                                                                                         Indels
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CUBPENT APPLICATION UNMER: 09/146,580 PRIOR APPLICATION NUMBER: 09/146,580 PRIOR FILING DATE: 1998-09-0 PRIOR FILING DATE: 1998-09-0 PRIOR FILING DATE: 1998-01-2 PRIOR APPLICATION NUMBER: 60/071,899 PRIOR FILING DATE: 1998-01-2 PRIOR APPLICATION NUMBER: 60/072,155 PRIOR APPLICATION NUMBER: 60/072,155 PRIOR FILING DATE: 1998-07-0 NUMBER OF SEQ ID NOS: 45 SOFTWARE: PALENTING PRIOR SEQ ID NOS: 45 SOFTWARE: PALENTING PRIOR SEQ ID NOS: 45 SOFTWARE: PALENTING PRIOR PRIO
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: Publication No. US200300497/5A1
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                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Detection and Treatment of Breast Cancer FILE REFERENCE: 3380/11127-UPG
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MOLECULE TYPE: pe
IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: MCP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-855-055 TELEFAX: 415-852-0155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA APPLICATION NUMBER: U
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CORRESPONDENCE ADDRESS:
ACTIVESSEE, Incyte Phaimaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 LESYT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
Local Similarity 100.0%;
es 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatities
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Pred. No.
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; ORGANISM: Homo sapiens US-09-834-795A-24

TYPE: PRT LENGTH:

Query Match

Local

h 100.0%; Score 25; DB Similarity 100.0%; Pred. No. 39; 5; Conservative 0; Mismatches

ps 10; Length 77;

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Indels

Matches

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US-10-033-067-1 RESULT 9

Sequence 1, Application US,10033067 Patent No. US20020164704Al

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Coleman, Boger
APPLICANT: Hilman, Jennifer L.
APPLICANT: Hilman, Jennifer L.
APPLICANT: HILMAN Jennifer
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: NOVEL HUMAN MONOCYTE CHEMCTACTIC PROPROTEIN
FILE REPERENCE: PF-0069-1 CON
FILE REPERENCE: PF-0069-1 CON
FILE REPERENCE: PF-0069-1 CON
FILE REPERENCE: PF-0069-1 CON
FILE REPERENCE: 1096-07-15
PRIOR APPLICATION NUMBER: 08/683.655

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LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (127)
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AFFLICANT: Find Peter
TITLE OF INVENTION: No.
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                                                                                                                                      US-09-895-913A-184
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                                                                                                         Sequence 184, Application US/09895913A Patent No. US20020160456A1
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                   APPLICANT: Kleanthous, Haidd
APPLICANT: Al-Garawi, Amel
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francoi
APPLICANT: Oomen, Raymond P.
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US-10-033-067-1

Matches

Ouery Match Best Local Similarity

Conservative

100 0%: Score 25: DB 100.0%: Pred. No. 55: U: Mismatches

рв 9: Length 109;

n; Indels

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SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 109

TYPE: PRT ORGANISM: Homo sapiens

NAME/KEY: misc\_feature OTHER INFORMATION: Incyte 10 No. 0820020164704A1 965817CD1

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US-09-754-858-875

Sequence 875, Application US/09764868 patent No. US20020168711A1

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
APPLICANT: ROSENTION: Nucleic Acids, Proteins, and Antibodies
TITLE of INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ 32
FILE REFERENCE: PTZ 32

CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510

SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 875 LENGTH: 151

ORGANISM: Homo sapiens

. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  $_{\rm US-09-754-868-875}$ 

TITLE OF INVENTION: Identification of Polynucleotides

Tomb, Jean Francois

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PRIOR FILING DATE: EARLIER FILING DATE: 177. PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FILING DATE: 1997-07-08 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: LARLIER FILING DATE: 1997-08-18 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
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GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: FARILIER APPLICATION NUMBER:
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: EARLIER APPLICAC
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PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 50/052,793
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
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TYPE: PRI
OPDANISM: Helicobacter pylori
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EARLIER FILING DATE: 1999-01-08
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                                   APPLICATION NUMBER: 60/055,723
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TITLE OF INVENTION: NOVEL PHYNOCLEOTIDES FILE PREPERAGE: 249-125
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FILE PREPERAGE: 249-125
FILE PREPERAGE: 249-126
CORRENT AFFLICATION HUMBER: JU-9-13-18
PRIOR APPLICATION NUMBER: JU-99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-09-0
SOFTWARE: PATENTIN VET: 3.0
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US-09-738-626-6675
Sequence 6675, Application Us/
/ Publication No. US200201976. A
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APPLICANT: NAKAGAWA
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LENGTH: 255
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PRIOP APPLICATION NUMBER: FARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIEF FILING DATE: 1997-09-12
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PRIOR FILING DATE: EARLIEF FILING DATE: 1997-09-12
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SENOH, AKIHIRO
IKEDA, MASATO
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DATE: 1997-08-18
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US-09-738-626-6675
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PRIOR APPLICATION NUMBER: US 60/197,747
PRIOR FILLING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US 60/197,747
PRIOR APPLICATION NUMBER: US 60/197,747
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,649
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,640
PRIOR APPLICATION NUMBER: US 60/207,640
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,961
PRIOR APPLICATION NUMBER: US 60/205,961
PRIOR APPLICATION NUMBER: US 60/205,961
PRIOR FILLING DATE: 2001-05-29
PRIOR FILLING DATE: 2001-05-29
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PRIOR APPLICATION NUMBER: US 60/207,506
PRIOR PRIOR PILLING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,506
PRIOR PILLING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 09/860,821
PRIOR PILLING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/860,821
PRIOR PILLING DATE: 2001-05-18
PRIOR PILLING DATE: 2001-05-18
PRIOR PILLING DATE: 2001-05-19
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Best Local Similarity
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APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL HUMAN 39228, 21956, 25856, 22244, 8701,
TITLE OF INVENTION: 50250, 55158, 47765, 62088, 50566, AND 48118
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/218,385
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/945,327
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/219,425
PRIOR APPLICATION NUMBER: US 60/318,581
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PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,650
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/907,509
PRIOR APPLICATION NUMBER: US 09/907,509
PRIOR FILING DATE: 2001-07-16
                                                                                SEQ ID NO 14
                                                                                                                                  PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 41
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                                                                                                         SOFTWARE: FastSEQ Version 4.0
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ORGANISM: Homo sapiens
                                              LENGTH: 467
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al Similarity 100.0%; Pred. No. 1.7e+02;
5; Conservative 0; Mismatch...
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US-10-160-501-14

Query Match
Query Match
Best Local Similarity 100.0% Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 248 LESYT 5
Db 248 LESYT 252

Search completed: April 8, 200 12:06:20

Search completed: April 8, 200 12:06:20
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C.

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st-processing: Minimum Match 08
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                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                       Score
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Query
Match Length DB
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   US-09-134-001C-3833
US-09-134-001C-3015
US-08-855-841-15
US-08-811-583-3
US-08-856-841-15
US-08-956-94-185-16
US-08-956-94-185-16
US-08-956-94-185-16
US-08-965-28-81-17
US-08-865-28-81-17
US-08-865-841-17
US-08-865-841-16
US-08-865-841-16
US-08-865-841-19
US-08-865-841-18
US-08-865-950-12
US-09-695-950-12
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Sequence 9, Appli
Sequence 15, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 18, Appl
Sequence 18, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 12, Appli
                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                 Sequence 3833, Ap
Sequence 3015, Ap
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RESULT 2 US-09-144-001C-3015  Sequence 3015, Application PS/09144001c  Pattent No. 6380370  GENERAL INFORMATION: RECEIVE AND AND ACID SEQUENCES RELATING TO STARBYLOCKE TYPE OF INVENTION: RECEIVE ACID AND THERAPEUTICS  TYPE OF INVENTION: RECEIVE ACID AND ACID SEQUENCES RELATING TO STARBYLOCKE TYPE OF INVENTION OF SEQUENCES AND THERAPEUTICS  CIPPERT AFELINATION UNMERS. US.60/054,964  PRIOR FILING DATE: 1997-08-13  PRIOR FILING DATE: 1997-08-14  PRIOR FILING DATE: 1997-08-14	Query Match  88.9%: Score (2) DB 4: Length 204; Best Local Similarity 71.4%: Pred. No. 12; Matches 5: Conservative 2; Mishitches (0) Indels (0) Gaps (0); Oy 1 IKEYFTS 7  111111: Pb 195 VKEYFTA 201	RESULT 1 US-09-134-001C-3833 Sequence 3833, Application US/091340010 Patent No. 6380370 GENERAL INFORMATION: AFFLICANT: Lynt Dougette-Stamm et al TIPLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: FILTHER TO STAPHYLOCOCC TITLE OF INVENTION: FILTHER TO STAPHYLOCOCC TITLE OF INVENTION OF THE STAPHYLOCOCC TOTHER AFFLICATION NUMBER: US-60/055.777 PRIOR AFFLICATION NUMBER: US-60/055.777	ALIGNMENTS	28 27 75.0 62 4 US-09 147 476 486 Sequence 14. Appl 30 27 75.0 66 1 US-08-387:11-14 Sequence 14. Appl 30 27 75.0 66 1 US-08-482-111-14 Sequence 14. Appl 31 27 75.0 67 1 US-08-3482-11 Sequence 2. Appl 32 27 75.0 68 2 US-08-946-387-1 Sequence 1. Appl 33 27 75.0 68 2 US-08-946-387-1 Sequence 17. Appl 35 27 75.0 68 2 US-08-946-387-1 Sequence 17. Appl 35 27 75.0 68 2 US-08-946-323-1 Sequence 17. Appl 36 27 75.0 68 3 US-08-46-323-1 Sequence 17. Appl 36 27 75.0 68 4 US-08-86-422-1 Sequence 17. Appl 39 27 75.0 68 4 US-08-86-422-1 Sequence 17. Appl 39 27 75.0 68 4 US-08-86-422-2 Sequence 2. Appl 40 27 75.0 68 4 US-08-86-422-2 Sequence 3. Appl 41 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 42 27 75.0 69 4 US-08-86-422-2 Sequence 5. Appl 42 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 43 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 43 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 44 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 44 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 44 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 45 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 45 27 75.0 69 4 US-08-86-422-2 Sequence 4. Appl 5. Appl 5. Appl 6. A
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ORGANISM: Staphylococcus epidermidis 09 \cdot 134 \cdot 001C \cdot 3015
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08-856-841-9
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                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: ATST - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 27,224
REFFENCE, COCKET NUMBER: LFF-4222-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: DE40038252
FILING DATE: 8-FEBRUARY-1990
AITORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER 05/08/856,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MANERED MO12
TITLE OF INVENTION: OR POLYPEPTIDES PROM THE PARVOVIRUS R19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                        FRAGMENT TYPE: INTERNAL ORIGINAL SOURCE: SERUM FROM PATIENT WITH ACUTE IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
                                                                                                                                                            DESCRIPTION: PEPTIDE HYPOTHETICAL: N/A ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/01
FILING DATE: 16-MARCH-1994
APPLICATION NUMBER: US 07/91
FILING DATE: 4-AUGUST-1992
APPLICATION NUMBER: PCT/0F91
FILING DATE: 8-FEBRUARY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                       FEATURE
                                                                                       POSITION IN GENOME: N/A
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                        LINEAR
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8-FEBRUARY-1991
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UMBER: US 07/917.096
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 mass spectrometry
                 amino acid analysis and
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Pred. No. 2.1e+02:
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US-08-811-583-3
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                                                                                                                                                                                                                                                            : Sequence 3, Application US/08811583 : Patent No. 6218142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.8%: Score 47.8est Local Similarity 66.7%: Pred. N.
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AUTHORS: COSSART, Y.E.
AUTHORS: FIELD, A.M.
AUTHORS: CANT, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
AUTHORS: MANIATIS, T.
AUTHORS: FRITSCH, E.F.
AUTHORS: SAMBROOK, J.
                                                                                         APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MODERNIES ENCOTING
TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
TITLE OF INVENTION: RNA-DIRECTED RNA FOLYMERASE (RdRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
PUBLICATION INFORMATION:
                 COPPRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americus
                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                      194 VKDYFT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: SMITH, D.B.
AUTHORS: JOHNSON, K.S.
AUTHORS: JOHNSON, K.S.
TITLE: SINGLE STEP PURIFICATION OF POLYPEPTIDES
TITLE: EXPRESSED IN ESCHERICHIA COLI AS FUSIONS WITH
TITLE: GLUTATHIONE S. TPANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: CANT, B.
AUTHORS: WIDDOWS, D.
TITLE: PARYOVIPUS-LIKE PARTICLES IN HUMAN SERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VOLUME:
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1975
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New York
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MOLECULAR CLONING
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STATE: New York COUNTRY: USA

10020

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rs-08-856-841-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-595-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSJEM: PC-LucyMS-FOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT6T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SCETWAKE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27.7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEPTIDES TITLE OF INVENTION: OF POLYPEPTIDES FROM THE PARVOVIRUS B19 NUMBER OF SECUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ERWIN SOUTSCHEK APPLICANT: MANFRED MOTZ
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                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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            APPLICATION NUMBER: PTT/EP1/99/
FILING DATE: 8-FEBRUARY-1991
APPLICATION NUMBER: DE40038262
FILING DATE: 8-FEBRUARY-1990
                                                                                       APPLICATION NUMBER:
FILING DATE: 4-AUGU
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: NEW YORK
STATE: NY
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                                                                                                                                  APPLICATION NUMBER: US/OR/7
FILING DATE: 16-MARCH-1994
                                                                                                                                                                                                                              APPLICATION NUMBER: US, 008, 0856, 841
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4-AUGUST-1992
UMBER: ECT/CE91/00106
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; PUBLICATION DATE: ; RELEVANT RESIDUES IN SEQ ID NO: US-08-856-841-15
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                                                                                                                                                               FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 1°:
RUBLICATION INFORMATION:
AUTHORS: SMITH, D.B.
AUTHORS: JOHNSON, K.S.
TITLE: SINGLE STEP PUBLIFICATION OF FOLYPEPTIDES
TITLE: EXPRESSED IN ESCHERICHIA COLI AS FUSIONS WITH
IITLE: GLUTATHIONE S. TRANSFERASE
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KEFERENCE/DOCKET NUMBER: LKR-9222-A
TELECOMMUNICATION INFORMATION:
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PUBLICATION INFORMATION:
AUTHORS: COSSAPT, Y.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPIGINAL SOURCE: SERMM FROM PATIENT WITH ACTIVE OPIGINAL SOURCE: IMPECTION (ENTHEMA INFECTIOSIM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE:
PAGES: 72 - 73
DATE: 1975
                                                                                                                  VOLUME:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                 PAGES:
DATE:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 15:
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                                                  FILING DATE
                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                  DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               TITLE: MOLECULAR CLONING JOURNAL: COLD SPRING HARBOR, NY
                                                                                                  PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  ISSUE:
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                                                                                                                                                  TOURNA! .
                                                                                    1988
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(212) 557-5635
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DB 4: Length 227;

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Sequence 12, Application US/08856841 Patent No. 6274307 GENERAL INFORMATION:
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Best Local Similarity 66.7%;
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APPLICATION NUMBER. US/08/214,658
FILING DATE: 16-MARCH-1994
APPLICATION NUMBER: US 07/917,096
FILING DATE: 4-AUGUST-1992
APPLICATION NUMBER: PCT/DE91/U01U6
FILING DATE: 8-FEBRUARY-1991
                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER PEADABLE FORM:
MEDIDA TYPE: 3.5" FUPPY DISC
COMPUTER: AIST - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ERWIN SOUTSCHEK
APPLICANT: MANFRED MOTZ
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEPTIDES
TITLE OF INVENTION: OP POLYPEPTIDES FROM THE PAPVOVIRUS B19
                                                                                                                                  FRAGMENT TYPE: INTERNAL
OPIGINAL SOUPCE: SERUM FROM PATIFNT WITH ACUTE
ORIGINAL SOURCE: INFECTION (ERYTHEMA INFECTIOSUM)
IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE40038262
FILING DATE: 8 FEBRUARY-1990
ATTORNEY_AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGERPATION NUMBER: 27.224
REFERENCE_CC-CASE NUMBER: LKF-5222-A
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER "S
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                                                                                                                                                                                                                                        HYPOTHETICAL: N, ANTI-SENSE: N/A
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DESCRIPTION: PEPTIDE
OTHER INFORMATION: PUBLICATION INFORMATION:
                                                                                                                       FEATURE:
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COUNTRY:
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STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE.
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                                   NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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(212) 557-5635
                                                                                                                                                                                                                                                                                                                      LINEAR
                                                                                                                                                                                                                                                             N/A
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8-FEBRUARY-1991
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                                     mass spectrometry
                                                          amino acid analysis and
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Pred. No. 1e+02:
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APPLICANT: Furuichi, Yasuhiro
APPLICANT: Kimura, Hitoshi
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Kayasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITILE OF INVENTION: BIOTIN BIOSYNTHETI: GENES
FILE REFERENCE: Biotin Genes
CURRENT APPLICATION NUMBER: US/08/935,263A
CURRENT FILING DATE: 1997-09-22
                                                                                                                                                                                                                                                                                                                  US-08-935-263-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-856-841-12
EARLIER APPLICATION NUMBER: EP 96115540.5
EARLIER FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Sequence 16, Application US/08935263A Patent No. 6117669
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO: 12:

PUBLICATION INFORMATION:

AUTHORS: SMITH, D.B.

AUTHORS: JOHNSON, K.S.

TITLE: SINGLE STEP PURIFICATION 4F FOLLYPEFTIDES

TITLE: SINGLE STEP PURIFICATION 4F FOLLYPEFTIDES
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          200 VKDYFT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSN: 51
PAGES: 51
1988
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AUTHORS:
AUTHOPS:
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MOLECULAR CLONING
AL: COLD SPRING HARBOR, NY
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S: WIDDOWS, D.
PARVOVIRUS-LIKE PARTICLES IN HUMAN SERA
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Query Match
Best Local Similarity
Tatches 4: Conserve
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IS-09-594-185-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Kurthia sp.
IS-09-594-185-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Kurthia sp. 15-08-935-263-16
                                                                                                                                                                                                                                                                                                                                                                                                              S-08-605-284B-18
                                                                                                                                                                                                                                                                                                                                                                   sequence 18. Application US/08605284B Patent No. 6060271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 16
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: WALEWAYI, JOSE L
APPLICANT: RECIO-PINTO, ESPERANZA
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Furuichi, Yasuhiro
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE REFERENCE: Biotin Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 08/935,263
PRIOR FILING DATE: 1997-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR EPPLICATION NUMBER: EP 96115540.5
PRIOR FILING DATE: 1996-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/594,185
CURRENT FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 276
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                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 VREFFTS 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 77.8%; Score 28: Local Similarity 57.1%; Pred. No. 1
                                                                                                                               ZIP:
 APPLICATION NUMBER:
                                                                                                                                              COMMTRY.
                                                                                                                                                                    STATE:
                                                                                                                                                                                                                          ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IKEYFTS 7
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                                                                                                                               14603
                                                                                                                                                                                   ROCHESTER
                                                                                                                                                                  NEW YORK
                                                                                                                                                                                                     E: NIXON, HARGRAVE, DEVANS & DOYLE LLP CLINTON SQUARE, P.O. BOX 1051
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                                                                                                                                      USA
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US/08/605,284B
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has 0; Indels
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; Sequence 17, Application US/08856841
; Patent No. 6274307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overy Match 77.8%, Score 28: DB 8: Length 311: Best Local Similarity 71.4%; Pred. No. 1.4e+(2: Marches 5: Conservative 1: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ERWIN SOUTSCHEK
                    INFORMATION FOR SEQ ID NO: 17:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HALDT HAFFNER & DELAHUNTY
                                                                                                                                                                        FILING DATE: 8-FEBRUARY-ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: "S FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ERWIN SOUTSCI
APPLICANT: MANFRED MOTZ
TITLE OF INVENTION: IMMI
TITLE OF INVENTION: OR I
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MOLECULE TYPE: protein
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NAME: BRAMAN, SUSAN J.
SEQUENCE CHARACTERISTICS:
                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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TELEPHONE: 716-263-1636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
COUNTRY.
                                                      TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
                                                                                                                 PEGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-922.:A
                                                                                                                                  NAME: ROBINSON, WILLIAM R. PEGISTRATION NUMBER: 27,22
                                                                                                                                                                                        APPLICATION NUMBER: DE400382
FILING DATE: 8-FEBRUARY-1990
                                                                                                                                                                                                                                                   FILING DATE: 4-AUG
AFFLICATION NUMBER.
                                                                                                                                                                                                                                                                                                          AFPLICATION NUMBER FILING DATE: 16-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS Version 5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 99 PARK
CITY: NEW YORK
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STRANDEDNESS: not
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REGISTRATION NUMBER: 1950(28-1) (CRE D-1705)
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CLASSIFICATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 17:
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME.
                                                                                                                                                                                                                                                                  AUTHORS: SMITH, D.B.
AUTHORS: JOHNSON, K.S.
TITLE: SINGLE STEP PURIL
TITLE: EXPRESSED IN ESCI
TITLE: GLUTATHIONE S. T.
JOURNAL: GENE
201 VKDYFT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: CANT, B.
AUTHORS: WIDDOWS, D.
TITLE: PARVOVIRUS-LIKE PARTICLES IN HIMAN SERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: PEPTIDE POTHETICAL: N/A
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: MANIATIS, T. AUTHORS: FRITSCH, E.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 1975
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE: 1982
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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                                                                           Local Similarity
                                                                                                                                                       FILING DATE: PUBLICATION DATE:
                                                                                                                                                                                      DATE: 1988
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE
                                                                                                                                                                                                                                                       VOLUME:
                            1 IKEYFT 6
                                                                                                                                                                                                                                     ISSUE
                                                            4
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MOLECULAR CLONING
L: COLD SPRING HARBOR, NY
                                                                                                                                                                                                                                                                    GLUTATHIONE S. TRANSFERASE
                                                                                                                                                                                                                                                                                                   SINGLE STEP PURIFICATION OF POLYPEPTIDES EXPRESSED IN ESCHERICHIA COLI AS FUSIONS WITH
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VDE: INTERNAL
SERIM F
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                                                                Conservative
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                                                                             77,8%;
66.7%;
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                                                                           Score 28,
Fred. No.
                                                                Mismatches
                                                           1.8e+02;
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                                                                                            Length 387;
                                                                Indels
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US-08-856-841-19
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                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: N/A
ANTI-SENSE: N/A
ANTI-SENSE: INTERNAL
TYPE: INTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LK!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 8-FEBRUARY-1990
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEPTIDES TITLE OF INVENTION: OR POLYPEPTIDES FROM THE PARVOVIRUS B19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ERWIN SOUTSCHEK APPLICANT: MANFRED MOTZ
                                                                                                                                                                 PUBLICATION INFORMATION: ANTHORS: COSSAPT, Y E.
                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: SERUM FROM PATIENT WITH ACUTE
ORIGINAL SOURCE: INTECTION (ERYTHMA INTECTIOSUM)
IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME: N/A
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COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
TELEFAX: (
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CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/91
FILING DATE: 4-AUGUST-1992
APPLICATION NUMBER: PCT/DE91
FILING DATE: 8-FEBRUARY-1991
APPLICATION NUMBER. DE400382
           ISSUE:
                                                                                                                                                                                                                       LOCATION N/A IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 16-MARCH-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/856,841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMI
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                                                   VOLUME: I
                                                                                                        AUTHORS: CANT, B. AUTHORS: WIDDOWS, D.
                                                                                                                                                                                                         OTHER INFORMATION:
                                                                   JOURNAL:
                                                                                                                                                  AUTHOPS:
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1975
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                 72 - 73
                                                                                        PARVOVIRUS-LIKE PARTICLES IN HUMAN SERA
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                                                                       LANCET
                                                                                                                                              FIELD, A.M.
                                                                                                                                                                                                                                                                                N/A
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S-08-856-841-16
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Best Local :
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IAM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
           FRAGMENT TYPE: INTERNAL
FRAGMENT TYPE: SFROM FROM PATIENT WITH ACUTE
OPIGINAL SOURCE: INFECTION (EPYTHEMA INFECTIOSUM)
IMMEDIATE SOURCE GENERICALLY ENGINEERED PEFTIDE
POSITION IN GENOME: N/A
                                                                                                   MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                 REPERENCE, TARKET MARKET TARKETERNOUS TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPAX: (212) 557-5635
TELEFAX: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ERWIN SOUTSCHEK
APPLICANT: MANFRED MOTZ
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEPTIDES
TITLE OF INVENTION: OF POLYPEFTIDES FROM THE PAPVOVIENS FIR
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 8-FEBRUARY-1990
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTPATION NUMBER: 27 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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FEATURE:
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FILING DATE: 8-FFRBMANN
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STATE: NY
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                   TOPOLOGY:
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UMBER: US 07/8
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66.7%;
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Pred. No. 2.3e+02;
2; Mismatches 9;
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Query Match
Best Local Similarity
Watches 4, Conserva
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# Patent No. 6274307
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ERWIN SOUTS-LAL...

APPLICANT: MANPRED MOTZ

TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEPTIDES

TITLE OF INVENTION: OF POLYPEPTIDES FROM THE PARVOVIRUS BIS

NUMBER OF SEQUENCES: 28

OURRESPONDENCE AFORESS:

ADDRESSEE: BROOKS HAIDT HAFFNER & SELAHUNIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
AUTHORS: MANIATIS, T.
AUTHORS: FRITSCH, E.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
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VOLUME:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 15:
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DATE:
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AUTHORS: CANT, B.
AUTHORS: CANT, B.
AUTHORS: MILDOWS, D.
TITLE: FARVOVIRUS-LIKE PARTICLES 'N HUMAN SERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION
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RELEVANT RESIDUES IN SEQ ID NO: 1+:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE: SINGLE STEP PURIFICATION OF POLYPEPTIDES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: SMITH, D.B.
AUTHORS: JOHNSON, K.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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MOLECULAR CLONING
L: COLD SPRING HARBOR, NY
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66.7%;
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Pred. N : 2.4e-02:
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CITY: NEW YORK

202 VKDYFT 207

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FILING DATE: 8-FEBRUARY-1990
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON WILLIAM R.
REGISTRATION NUMBER: 27.224
REFERENCE/POCKET NUMBER. LKR-9222-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPHONE: (212) 697-365
                                                Matches
                                                                                 Query Match
                                                                                                                       -08-856-841-18
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PPIOP APPLICATION DATA:
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FRAGMENT TYPE: INTERNAL
OPIGINAL SOUPCE: SERUM FROM PATIENT WITH ACUTE
ORIGINAL SOUPCE: INFECTION (ERYTHEMA INFECTIOSUM)
IMMEDIATE SOUPCE: GENETICALLY ENGINEERED PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: COSSART, Y.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                         AUTHORS: FIELD, A M
AUTHORS: CANT, B.
AUTHORS: WIDDOWS D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                 y Match 77.8%;
Local Similarity 66.7%;
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 18:
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VOLUME: I
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                                                4; Conservative
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                                                    Mismatches
                                                                   Score 28; DB 4;
Pred. No. 2.4e+02;
                                                                                     DB 4; Length 501;
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; TYPE: PRT; ORGANISM: Citrus navelina var. class : US-09-413-452-2
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                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.8%; Score /H; DB 3; Length 584; Best Local Similarity 83.3%; Pred. NJ: 2.9e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PROCESS FOR STABILIZING PROTEINS IN AN TITLE OF INVENTION: ACIDIC ENVIRONMENT WITH A HIGH-ESTER PECTIN FILE PERFERNCE: DYOULA OULARD CURRENT APPLICATION NUMBER: US/04/413,452 CURRENT FILING DATE: 1999-10-06 EARLIER APPLICATION NUMBER: 08/983364 EARLIER APPLICATION NUMBER: 08/983364
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                                                                                          Matches
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 CUERENT APPLICATION NUMBER: US/00/413 468 CURRENT FILING DATE: 1999-06-06 EARLIER APPLICATION NUMBER: 08/983364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kreiberg, J.
APPLICANT: Buchholt, H.
TITLE OF INVENTION: PROFESS FOR STABLIZING PROTEINS IN AN
TITLE OF INVENTION: ACIDIC ENVIRONMEN: WITH A HIGH-ESTER PECTIN
FILE REFERENCE: DYOHA ONLARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Christensen, T. APPLICANT: Thorsoe, H.
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learch completed: April 8. 2003, 12:05:53
lob time : 23.5833 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Maximum Match 1008
Listing first 45 summaries
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# SUMMARIES

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InterPro: IPR000436; Sushi_S
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Pfam; PF00094; sushi; 1.
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Pf000m; PD000918; Link; 2.
SMART: SM00034; CCECT; 1.
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MEDLINE-93300846; PubMed-9314802;

Shinomura T., Nishida Y., Ito K., Kimata K.;

"CDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during chondroyenesis in chick limb buds. Alternative spliced multiforms of PG-M and their relationships to versican.";

J. Biol. Chem. 268:14461-14469(1993).

--- FUNCTION: May play a role in intercellular matrix. May take part connecting cells with the extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutes. There are no restrictions on it modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.is) sites, and or send an email to licensealsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY. CONTAINS I IMMUNOGLOBULIN-LIKE V-TYFE DOMAIN
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-!- SIMILARITY: CONTAINS 4 EGY-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYFE LECTIN FAMILY COMAIN.
-!- SIMILARITY: CONTAINS 1 SUSHI (SCP) DOMAIN.
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Eukaryota; Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi,
Archosauria: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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InterPro: IPR000742;
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PROSITE: PS01187: EGF_CA: 1.
PROSITE: PS01241: LINK: 2.
PROSITE: PS01241: LINK: 2.
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TC1_DICOL

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159_YEAST

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C P40477;
C P40477;
T 01=FEB-1995 (Rel. 31, Created)
T 16-OCT-2001 (Rel. 40, Last annotation update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
N NCP159 OF RAT7 OR YILLIGO.
N NUP159 OF RAT7 OR YILLIGO.
S Saccharomyres cerevisiae (Buker's yeast).
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable RNA 3'-terminal phosphate cyclase (EC 6.5 1 4) (PNA-3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMRL outstation the European Bioinformatics lustitute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a liberar processor (See http://www.isbosib.che.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF020279; AAB70847.1; -. DictyDb; DD02222; -.
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Eukaryota: Mycetorua: Clotyosteliida: Flotyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligase: Nuclear protein.
ACT_SITE 354 354
SEQUENCE 433 AA: 47110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF01137; RTC; 1. PR0SITE: PS01287; RTC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000228: RNA3'_term_cycl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate cyclase) (RNA cyclase).
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                                                                                                                                                                                                                                                                                                                                                             228 IKSYFTS 234
                                                                                                                                                                                                                                                                                                                                                                                                                     1 IKEYFTS 7
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CAUTION: THE C-TERMINAL SECTION OF THIS PROTEIN COULD BE INCOPPRET AND THE REAL PROTEIN IS PROBABLY SHORTER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB:
Pred. No. 30;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAFFBC044458CE9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 433;
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Query Match
Best Local Similarity
Thickes 5. Conserve
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                                                                                                                                                                                           PTKA_ECCLI
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                                       PTKA_ECOLI STANDARD: PRT: 150 AA.

P37187; P76413;
01-OCT-1994 (Rel. 30, Created)
01-NOV-1997 (Rel. 35, Last sequence spoke)
15-JUN-2002 (Rel. 41, Last unbotation update)
15-JUN-2002 (Rel. 41, Last unbotation update)
PTS system, yalactitod-specific IIA component (EliA-GAT) (Galacticol-permease IIA component) (Phosphotrans(crease enzyme II A component)
(EC 2.7-1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell BG., Badcock K., Bankler A.T., Bowman S., Brown D.,
Barrell BG., Badcock K., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Rint S., Jayels K., Jones M.,
Louis E., Lye G., Moule S., Moule 1. Odell C., Pearson D.,
Pajandream M.A., Piles L., Powley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.,
Submitted (EDY-1444) to The EMBLAND MAINTAIN (EDY-170FLASMIC EXPORT OF
                                                                                                                                                                                                                                                                   1190 LKEYYTS 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA AND ALSO IN FROTEIN IMPORT

-!- SUBBURIT: INTERACTS WITH DBP5.
-!- SUBCULLULAR LOCATION: Nuclear pare complex.
-!- DYMAIN: COMTRAINS A CENTRAL REGIAN WITH REPEATS THAT ARE X-X-F-G.
-!- DYMAIN: COMTRAINS A CENTRAL REGIAN WITH REPEATS ARE EMBEDDED

WITH IN 3 NEAPLY PEPFECT 26 ANN NO ACID TANDEM REPEATS.
Escherichia coli, and
Escherichia coli 0157:H7
                               GATA OR B2094 OR Z3257 OR ECS2897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; Transport; Repeat.

DOMAIN 518 617 4 X 27 AA TANDEM REPEATS.

REPEAT 518 543 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: L40634: AAC41652 1; -.
EMBL: 738128: CAA86265.1; -.
PIR; S48457: S48457.
SGD: S0001377: NUFLSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib-ch/announce/or send an email to license@isb-sib-ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorsch L.C., pockendorff T.C., Cole P.N.;
"A conditional allele of the novel repeat-containing yeast
mucle-pointm RATT/NUP159 causes both rapid cessation of mRNA export
and reversible clustering of nuclear pore complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLLINE=95263675; PubMed=7744966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaec.m; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interprop IPR004325; Nucleoporin_F0 fire FF34744 North-pringF3 19.
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                                                                                                                                                                                                                                                                                                     1 IKEYFTS 7
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570 5
596 6
1460 AA;
                                                                                                                                                                                                                                                                                                                                        Conservative
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595
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                158907 MW;
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STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Tilda T., Takami H., Honda T., Sasakawa G., Oyasawara N., Yasunaya T.,

Kuhara S., Shiba T., Hattori M., Shindyawa H.,

Complete genome sequence of enterohemorrhagic Eacharichia coli

Ol57:H7 and genomic comparison with a laboratory strain K-12.";

NAM Race R.11-29/20047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Filey M., Collado-Vides J. Glasner T.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nobelmann B., Lenyeler J.W.; "Sequence of the gat operon for galactitol utilization from a wild-type strain EC3132 of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna N.T., Piunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor T., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN+K12 / MG1655;
MEDLINE+97426617; PubMed+9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria: Protechacteria:
Escherichia:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=0157:H7 / EDD933 / ATCC 700927, MEDLINE=21074935; PubMed=11205551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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STRAIN-0157:H7 / N
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                                      EcoGene: EG12414: gatA.
InterPro: IPRO217 8: PSI_EIIA_2: 1.
Pfam: PF00359: PTS_EIIA_2: 1.
ProDom: PD001689: PTS_EIIA_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb/sib/ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL cutstation \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of enterchaemorrhagic Escherichia coli 0157.H7.":
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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Phosphotransferase system; Sugar transport; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to licenseelsb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYPHIVATE-DEPENDENT SUGAR PHOSPHOTPANSFERACE SYSTEM (PTS). A ANAOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE LICE COMAINS CONTAIN THE STGAR BUNGING STREE AND THE TRANSMEMBRANE CHANNEL: THE LIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOE IS PHOSPHOTHER): IIA IHANSFERS LIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  histidine + sugar phosphate.
SUBCELLULAR LUCATION: Cytoplasmic.
SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                               X79837; CAA56228.1; -. AE000298; AAC75155.1; -. AE0005435; AAG57151.1; -. AP002560; BABR6320 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8:11-22(2001)
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                                                                            Best Local
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Galactitol metabolism; Complete proteome CONFLICT 124 124 D -> E (IN REF. 1). SEQUENCE 150 AA; 16907 MW; 1A760076BESFB61D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Created)
Aspartate carbamoyltransferase 1, Chloroplast procursor (EC 2.1.4.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYB1_PEA
Q43086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots: Rosidae: eurosids I, Fabales, Fabaceae, Papilionolideae; Viclede) Pisum.
                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see hit; ...www.isb-sit-oblanch-coeffor send an email to license@isb-sib-ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Wando; TISSUE-Leaf; MEDLINE-94402176; PubMed-8029359; Williamson C.L., Slocum R.D.;
                                                                                                                                                                                                                                                     InterPro: IPR002029: Asp,Orn_Cotrant.
InterPro: IPR002082; Asp_carbmltransf.
pfam: PF00185; OTCace; 1.
pfam: PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and characterization of the pyrBl and pyrB2 qenes
encoding aspartate transcarbamoylase in pea (Pisum sativum L.).";
Plant Physiol. 105:377-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pisum sativum (Garden pea)
                                                                                                                            SEQUENCE
                                                                                                                                             CHAIN
                                                                                                                                                                                                         TIGREAMS; TIGRO0670; asp_carb_tr: 1
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                        EMBL; M96981; AAA62443.1; HSSP; P00479; 3CSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3888;
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                                                                                                                                                           TRANSIT
                                                                                                                                                                          Multigene family.
                                                                                                                                                                                           Pyrimidine biosynthesis; Transferase; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                         PRINTS; PROOIDO; ACTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Aspartate transcarbamylase 1) (ATCHSe 1).
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 275 IKEYLTS 281
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                              1 IKEYFTS 7
                                                                            Similarity
                                                                                                                            386 AA;
                                                             Conservative
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                                                                                                                            386 ASPARIATE CARBAMOYLTRANSI
42617 MW, A9440F45474E29F4 CRC64
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83.3%;
                                                                              83.3%;
85.7%;
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                                                                           Score (1) DB
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40
                                                                                                                                                            CHLORGINAST (POTENTIAL)
                                                               Mismatches
                                                                                                                                             CARBAMOYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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ANB_PIRSP
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T 01-OCT
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ANC_PIRSP
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                                                                                                            ESULT 8
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SIGNAL
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Mannan endo-1,4-bera-mannosidase C precursor (EC 3.2
mannanase C) (1,4-beta-D-mannan mannanohydrolase C).
                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evidence that the Piromyces gene family enceding enderl.4-mannanases arose through gene duplication".
FEMS Microbiol Lett. 141:183-188(1996).
-I- CATALYTIC ACTIVITY: Kandom hydrolysis of 1,4-beta-D-mannosidic linkages in mannans, galactomannans, glucomannans, and
01-0CT-1996 (Rel. 34. Created)
01-0CT-1996 (Rel. 34. Last sequence update)
15-0CL-1998 (Rel. 36. Last amoutation update)
Nannan endo 1.4-beta-mannosidase B precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002883; CBD_5.
InterPro; IPR000805; Glyco_hydro_26
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities regulies a license agreement (See http://www.ish-sib ch/announce/or send an email to license@ish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-96313314; PubMed-8768520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neocallimasticaceae: Piromyces. NCBI_TaxID=45796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P55298;
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                                                                              MANB_PIRSP
                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00739; GLHYDRLASE26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X97520; CAA66134 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Millward-Sadler S.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piromyces sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES
                                                                                                                                                       444 LKEYFT 449
                                                                                                                                                                                                                               Local similarity
                                                                                                                                                                                     1 IKEYFT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactoglucomannans.
SIMILARITY: THE 39 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANC
AND XYNA; AND TO THOSE OF N.PATRICIARUM XYNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              PF02013; CBM_10; 2.
PF02156; Glyco_hydro_26; 1.
                                                                                                                                                                                                                                                                               480
569
                                                                                                                                                                                                                                                                                                                                                                                     Glycosidase: Signal: Multigene family: Repeat.
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                AA:
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477
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                                                                                                                                                                                                                                                                               64115 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall J., Black G.W., Hazlewood G.P.
                                                                                                                                                                                                                               Score 30; DB
                                                                                                                                                                                                                                                                               POLY-ASN.
; 19277764E18328B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                       MANNAN ENDO-1,4-BETA-MANNOSIDASE C 2 X 39 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                             POLY-ASN
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                                                                                                                                                                                                                 Mismatches
                                                                              571 AA
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                                                                                                                                                                                                                                                 DB 1: Length 569;
   (EC 3.2.1.78) (Beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   efesij
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PRESENTATION OF THE PRESEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 27.1 kDa protein UFD4 "API inter
YKL009W OR YKL160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PPOT entry is copyright it is produced through a collaboration between the Swiss Institute of Rio oformatics and the EMBL outstation the Ewropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes Saccharomycetales; Saccharomycetacoae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                              YKA9_YEAST
P33201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF02013; CBM_10; 2.
Pfam: PF02156; Glyco_hydro_26; 1.
PPINTS; PR00739; GLHYDPLASE26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arose through gene duplication."; FEMS Microbiol. Lett. 141:183-188(.795).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96313314; PubMed=8768520; Millward-Sadler S.J., Hall J., Pl
Pascolo S., Ghazvini M., Boyer J., Colleaux L., T
"The sequence of a 9.3 kb segment to ated on the
                                                           MEDLINE=93127732; PubMed=1481574;
                                                                                                                                                                               Saccharomycetales;
                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's ; east)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X97408; CAA66061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (set http://www.isb/sib-ch/dammines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piromyces sp.
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                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID=4932;
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InterPro: IPR002883; CBD_5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 LKEYFT 451
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SIMILARITY: BELONGS TO FAMILY 25 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactoglucomannans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Slycosidase, Signal; Multigene family: Repeat 1 19 POTENTIAL.
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533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Length 571; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ASN.
; Bl3F44581FAA9DAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANNAN ENDO-1, 4-BETA-MANNOSIDASE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 X 34 AA APPROXIMATE REPEATS
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      Thierry A., I
e left arm of
                                  Dujon B.;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yeast chromosome XI reveals five open reading frames including the CCEI gene and putative products related to MYO2 and to the ribusomal protein L10.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.ish-sib-bl/announce, or send an email to license sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents the statement is not removed.
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Yeast 9:279-287(1993
                                                                                                                                                     Nelson K.E. Clayton R.A. Gill S.R. Gwinn M.L. Dodson R.J., Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C. Ketchum K.A., McDonald L. Utterback T. R. Majek J.A. Linher K.D. Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eraser C.M., Salzberg S.L., Smith H.O., Venter J.C., Eraser C.M., Salzberg S.L., Smith H.O., Venter J.C., Eraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
36-MAY-2000 (Rel. 40, Last annotation update)
Heat-inducible transcription repressor hrea homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93∠5590¢; PubMed=¤48¤/∠¤;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 8:987-995(1992).
                 SAZMSÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRCA_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                  STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A STRAIN=MSB8 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S30013; S30013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO YEAST RIBOSOMAL PROTEIN L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barteria; Thermotogae; Thermotogae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRCA OR TM0851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001790; Ribosomal_L10
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 VKEYFKS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IKEYFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S0001492; YKL009W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z28009; CAA81844.1; -. S59773; AAC60552.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00466: Ribosomal_L10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x61398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S53418; AAB24904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOT_ANNOTATED_CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27058 MW.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9FCFDEE9F009F427 CRC64;
HRCA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (class); Thermotogales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 236; 42;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not semoved. Usage by an entities requires a license agreement (See http://www.istorsend.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PPOT entry is copyright it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _ACTS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01628; HrcA; 1.
TIGPFAMS; TIGR00331: hrcA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001751; AAD35933.1; -.
                                                                                               the European Bioinformatics Institute. There are no restrictions on model by non-profit institutions as instituted as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement the http://www.ish-sil.license.gisb-sil.ch).
                                                                                                                                                                                                                                                                                                                                                       "The AcbC protein from Actinoplanes species is a C7-cyclitol synthase related to 3-dehydroquinate synthases and is involved in the biosynthesis of the alpha-glucosidase inhibitor ararhose.";
J. Biol. Chem. 274:10889-10896(1999).
-i- FUNCTION: C7-cyclitol synthase using sedo-heptulose 7-phosphate, but not ido-heptulose 7-phosphate and 3-deoxy-arabino-heptulosonate 7-phosphate, as a substrate. Involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Fel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence apdate)
15-yin-2002 (Rel. 41, Last annotation update)
2-epi-5-epi-valiolone synthase (EC 4.2.3.-) (Sedo-heptulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; TM0851
                            InterPro: IPR002658; DHQ_synthase. Pfam; PF01761; DHQ_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Micromonosporineae: Micromonosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate cyclase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ZAE9;
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepersberg W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stratmann A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99214159; PubMed-10196166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinoplanes sp. (strain 50/110)
                                                                    EMBL; Y18523; CAA77208.1; 1.
                                                                                                                                                                                                                                                  -!- COFACTOR: NAD and a divalent notal cation such as cobalt.
               Lyase; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 LSEYFTS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                       inhibitor acarbose.
CATALYTIC ACTIVITY: Sedo-heptuisse 7-phosphate - 2-epi-5-epi-
                                                                                                                                                                                                                                                                                        valiolone +
                                                                                                                                                                                                                                                                                                                                           biosynthesis of the acarviose unifety of the alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002571; HrcA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AA;
382 AA; 42181 MW; EDA. 10044A14B88B3 TRC64.
               Cobalt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahmud T., Lee S., Distler J., Floss H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                        phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ation; Repressor
39306 MW; 02A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.6%; Score 24; DB 71.4%; Fred No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     esso: Heat shock; Compl
02A5-5A546C313AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    noved. Usage by and for (Sue hit; ) www isb-sib-o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1: Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete proteome.
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A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.
A Choi S. F. Codani I... Connerton I.F., Cummings N.J., Dancel R.A.,
A Choi S. F. Codani I... Connerton I.F., Cummings N.J., Dancel R.A.,
A Choi S. F., Codani I... Connerton I.F., Cummings N.J., Dancel R.A.,
A Choi S. F., Codani I... Fabret C., Ferrati E., Foulget D.,
A Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Hilbert H., Holsappel S., Hasonn S., Hullo M.F., Itaya M., Jones I.,
A Golis S.Y., Glaser P., Koningstein G., Krogh S., Kumano M.,
A Hilbert H., Holsappel S., Hardincis S., Lubber J., Lazarevic V.,
A Kurita K., Lapidus A., Lardincis S., Lubber J., Lazarevic V.,
A Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Madigua C.,
A Modina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
A Moone D., O'Peilly M. Oyawa K. Oylwara A. Oydega R., Pork S.H.,
A Noone D., O'Peilly M. Oyawa K. Oylwara A. Oydega R., Pork S.H.,
A Noone D., O'Peilly M. Oyawa K. Oylwara A. Oydega R., Pork S.H.,
A Ricqer M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Ricqer M., Senora S., Schroeter R., Scoffone F.,
A Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
A Schlighi M., Tanakshi A., Tanaka T., Terpstra P., Tognoni A.,
A Viari A., Waghur P., Wadher E., Wasarotti A.,
A Viari A., Waghur P., Wadher E., Wasarotti A.,
A Vishi A., Waghur P., Wadher E., Wasarotti A.,
A Vishi A., Waghur P., Wadher E., Yasameto K.,
A Winters F., Wigat A., Yamancho H., Wanner P., Wadher P., Vata F.,
A Winters F., Waller B., Cannella R., Valar P., Waller B., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ğ,
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                          use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a livense agreement (See http://www.ish.sib.ch/announce.com/send an email to licensealsb-sib.ch).
                                                                                                                                                                                                                                          This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics, and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 390-249-256(1997).

NATURE 390-249-256(1997).

-I- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUP AND SELENIUM ATOMS FROM I-CYSTEINE, L-CYSTINE, L-SELENOCYSTEINE, AND L-
       EMBL; Z99120; CAB15258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Probable cysteine desulfurase (EC 4.4.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98044033; PubMed-9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 5: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY). SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                      AMINOTRANSFERASES. CSD SUBFAMILY
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89.08
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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                                                                                                                                                                                                                                                                                                a rollaboration
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                                                                         Euery Match
Best Local
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Best Local
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                                                                                                                                  Hypothetical protein; Zinc-finger; INA-binding; Metal-binding; Nuclear protein; Repeat.

Nuclear protein; Repeat.

ZN_FING 46 68 C2H2-TYFE.

ZN_FING 73 98 C2H2-TYFE.

ZN_FING 103 126 C2H2-TYFE.

ZN_FING 103 126 C2H2-TYFE.

ZN_FING 317 340 C2H2-TYFE.

ZN_FING 317 340 C2H2-TYFE.
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-FROT entry is copyright it is produced through a collaboration between the Swiss Institute of Bidisformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions is long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oli-FEB-1996 (Rel. 33, Created)
Oli-FEB-1996 (Rel. 33, Last sequence indate)
10-OCT-2001 (Rel. 40, Last annotate update)
Hypothetical zinc finger protein F9-50 1 in chromosome II.
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                          PRINTS, PROCO48, ZINCFINGER,
SMART, SHOCKSE, CHP_CHD; 5.
PROSITE, PS50157, ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sin.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chissoe S., Wilson R.; Submitted (MFV 1995) to the EMHL/V-1994, FEBJ databases
                                                                                                                                                                                                                                                                                                                                                                    EMBL; U39997; AAA81101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukaryota: Metazoni Nematoda: Chromilorea: Rhabditida: Rhabditoideu:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00266; aminotran_5; 1. PROSITE; PS00595; AA_TRANSFER_CLAS: _5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subtifist; BG14009; csd.
                                                                                                                                                                                                                                                                                                                       Pfam; PP00096;
                                                                                                                                                                                                                                                                                                                                      :ca.jae.uc.
                                                                                                                                                                                                                                                                                                                                                      WormPep; F56D1.1; CE01969.
                                                                                                                                                                                                                                                                                                                                                                                                                 entities regulies a license agreement (See http://www.isb-sib-ch/announce)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear (Fotential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditidae: Peloderinae: Caenorha: fitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F56D1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P77444; 1JF9.
150 IKEYHTS 156
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                              1 IKEYFTS ?
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es 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyridoxal phosphate; Comple*+ proteome.
G 224 224 PYRIF*-XAL PHOSPHATE (BY SIMILARITY).
CE 406 AA; 44922 MW; E43-4-0-B5965349D1 CRC64;
                                                         l Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                       REBUCURANT
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                      50097 MW;
                                                                         85.7%;
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H2: 5.
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83.3%;
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Pred, No.
                                                                         Score 19; DE
Pred. No. 81;
                                                                                                                      240AA+95F75343D6 CRC64;
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                                                             Mismatches
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75;
                                                                                        DB 1: Length 435
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SULT 15
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Exchinulease ABC subunit C.
UVRC OR CPE0352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http.//www.isb'sib.oh/aumounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

-:- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAWAGED NUCLEOTIDE SECHENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). ATTACHES TO THE UVRA-UVRB COMPLEX. DISPLACING UVRA, AND THE DAWAGED DNA STRAND IS
004781: 004029;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 180.2 kDa protein in FAA4-HOR7 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiacede;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART: SM00465; GIYC: 1.
TIGREAMS: TIGR00194; uvrC: 1.
PROSITE: PS50151: UVR: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01541; Exci_endo_N; 1. Pfam; PF02151; UVR; 1. ProDom; PD005870; UVrC_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1502;
                                                                                                                                            YM81_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOS response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001943; UvrB/C.
InterPro; IPR004791; UvrC.
InterPro; IPR001162; UvrC_C.
InterPro; IPR000305; UvrC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP003186; BAB80058.1; -.
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PubMed-11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000445; HhH.
                                                                                                                                                                                                                                                                                  614 IKQYFSS 620
                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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SIMILARITY: CONTAINS 1 GVP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
620 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                            STANDARD;
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71390 MW;
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71.4%;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6ED4ADE9C3849219 CRC64;
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                                                                                                                                              1562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 AA.
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Job time : 19.9167 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Wa
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: STPONG, TO HUMAN ZNE294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
PROSITE: PS50089; ZE_RING_2; 1.
Hypothetical protein; Zinc-finger.
ZN_FING 1508 1555 RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMEL: 248639; CAAR8574.1; -.
EMBL: 248756; CAA88657.1; -.
SGD: SQN04861; YMP247C.
ThterPro: TP600184; Znf_ring.
SMART: SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hunt S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (MAR-1995) to the EMBL/GenHank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YMF247C OR YM9408.09C OR YM9920.01C
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 950-1562 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                            462 IEDYFTS 468
                                                                                                                                                                                                                                                                                                                Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                  1 IKEYFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1562 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                     71.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180185 MW; 97AC65E881362305 CRC64;
                                                                                                                                                                                                                                                                                                                        Mismatches
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GenCore version 5.1.4_p5_4578

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M protein - protein search, using sw model

un on: April 8, 2003, 11:59:15 ; Search time 30.9167 Seconds

(without alignments)

21 766 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues

otal number of hits satisfying chosen parameters. 283224

Inimum DB seq length: 0 aximum DB seq length: 2000000000

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2: pir2.\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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COMPLETION SINC Fin	probable DNA-direc	conserved hypothet	conserved hypothet	toxin secretion AT	hypothetical prote	hypothetical membr	hypothetical prote	nifS protein homol	Drosophila translo	gomplement control	heat shock operon	aromatic metabolit	Hypothetical prote	probable glucose-1	hypotherical prote	

### ALIGNMENTS

RESULT 2  T32922  T32922  P32922  hypothetical protein K09H9.5 - Caenorhab ditis elegans C.Species: Caenorhabditis elegans C.Pate: 29-Oct 1999 #sequence_revision /4-Oct-1999 #text_change 20-Oct-1999 C.Accession: T32922  R.Madsen, C.; Graves, T.; Blair, T.  submitted to the FMBL Data library. January 1998 A.Description: The sequence of C. elegans cosmid K09H9. A.Peference number: Z21247 A.Accession: T32922 A.Status: preliminary; translated from CACFMRI, TOPBJ A.Molecule type: DNA A.Fessidues: 1-466 -MAC. A.Gross: Leferences: EMBL AS043700 FIRD AAR07572.1, CSELB.CH00019, CEST.K09H9.5 A.Gross: Leferences: EMBL AS043700 FIRD AAR07572.1, CSELB.CH00019.5 A.Gene - CESP-K09H9.5 A.Map position: 1	Query Match 88,9%; Score 32; DB 2; Length 278; Hest Local Similarity 100 0%. Pred No. 29; Matches 6; Conservative 0; Missatches 0; Indels 0: Gaps 0; Oy 1 IKEYFT 6  Oy 1 IKEYFT 6  Db 163 IKEYFT 168	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-278 <arn> A;Residues: 1-278 <arno40 :dhs="" biosynthesis;="" c;keywords:="" c;superfamily:="" dihydropteroate="" domain:="" f;18-258="" folate="" homology="" synthase="" transferase=""></arno40></arn></arn></arn></arn></arn></arn></arn></arn></arn></arn>	RESULT 1 E72425 dibydropteroate synthase (EC 2.5.1.15) TM0.040 [similarity] - Thermotoga maritima (st C;Species: Thermoto	
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bmitted to the EMBL Data Library, May 1995.
Description: The complete sequence of a 40.7 kb segment located on the left arm of east hypothetical proteins.
Reference number: $55159
Accession: $55167
                                                                                                                                   Molecule type, DNA Residues: 1-268, F. 269-281, F. 283-460, W., 762-460 ASIA Gross-refarences EMBL M21726, NID.3845073, FID 3885074 Katsoulou, C.) Tzermia, M.; Alexandraki, D. bmitted to the Protein Sequence Database, September 1995 Reference number: 856912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: 08-Jul-1995 *sequence_revision 01-Sep-1995 *toxt_chingo 21-Jul-2000 Accession: $55167: $55718: $56928; $71651 Katsoulou. C.: Tzermia. M.- Alevandraki n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2-dependent signaling protein - yeast (Saccharomyces cerevisiae)
Alternate names: protein J0642: protein YJL146w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Sus scrofa domestica (domestic pig)
Date: 04.het/1997 #sequence_tevision 04.het/1997 #text_clange 10.cdt/1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                        Sia, R.A.; Mitchell, A.P.
bmitted to the EMBL Data Library, February 1995
Description. A novel gene, IDS2, is required for IME2 dependent functions.
Reference number: S55718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168-182/Region: CMP-N-acetylneuraminic acid binding
186-206/Region: cytochrome b5 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Experimental source, submandibular gland
Keywords: 2Fe-2S; cytosol; iron-sulfur protein; monomer; NAD, oxidoreductase
53-58,389-395/Region: iron binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-415 <SCH>
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                  Katsoulou,
                                           Cross-references: EMBL:Z49421; NID:gl015558; PID:gl015559; MIPS:YJU146w
                                                                   Molecule type: DNA
Residues: 1-469 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:X87371; NID:g854542; PID:g854551
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-469 <KAT>
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                                                                                                                      Accession: S56928
                                                                                                                                                                                                                                                                                                        Accession: S55718
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787-797,
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                  Tzermia, M.; Tavernarakis, N.; Alexandraki,
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100.0%; Fred. No.
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    Mismatches

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Query Match
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RECHambaud, I.; Heilig, R.; Ferris, S.; Harbe, V.; Samson, D.; Galisson, F.; Moszer, Rucheic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Aeression: F90875
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A; Residues: 1-469 < KAF>
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A;Accession: $71651
A:Status: nucleic_acid_sequence nut_shown_translation_not_shown
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                                                                                                                                                                                                                                                                                                                                                                 lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 *sequence_revision 24-May-2001 *text_change 03-Aug-2001 C;Accession: E90575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kawano, T.: Koyama, S.: Takematsu, H.: Kozutsumi, Y.: Kawasaki, H.: Kawashima, S.: J. Biol. Chem. 270, 16458-16463, 1995
A:Title: Melecular clopshy of cythdine "hosphospho-Newscylpeuraminic acid hydroxylas A;Reference number: A57469, MUID:95332342; PMID:7608218
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C; Genetics:
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A;Status: preliminary; not compared with conceptual translation
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                                          A; Genetic code: SGC3
                                                                 A; Gene: MYPU_5090
                                                                                                                 A; Experimental source: strain UAB CTIP
                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-620 < KUR>
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A;Cross references
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A; Residues: 1-577 <KAW>
                                                                                                                                              A;Cross-references: GB:AL445566; PID:gl4:089423; PIDN:CAC13682 l: GSPDK:GN00153
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ilarity 100.0%; Pred. No.
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Score 52;
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49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :Hammerschmidt, M.; Nusslein-Volhard, C. evelopment 119, 1107-1118, 1993
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1264-345; Commain. Link protein repeat bomology SINKI.

13178-1253; Domain. EdF homology EDF1.

13298-1253; Commain. EdF homology EDF1.

13298-1327; Commain. EdF homology EDF1.

13298-1327; Commain. Crtype leath bomology SICH.

13461-3517; Commain. Crtype leath bomology SICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 )Status: preliminary, translated from GB/EMBL/SUBJ
;Molecule type, mank
;Residues: 1-260 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: 150109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Brachydanio rerio (zebra fish)
;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Status: preliminary
;Molecule type: nucleic acid
;Residues: 1-3562 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Title: cDNA cloning of PG-M, a large chandroitin sulfate proteoglycan expressed during
                                                                                                                                                                                                                                                                                                                                                   :Gene: sna-l
                                                                                                                                                                                                                                                                                                                                                                                 ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :Title: The expression of a sebrafish gene bomplopous to Drosophila small suggests
:Reference number: I50109: MUID:94139555; PMID:8306877
                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X74790; NID:g468620; PID:g468621
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                    71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%; Score 32; DB 2; Length 3562; 100.0%; Pred. No. 4e+02;
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1; Mismatches
                                                                                                                                                                                                                                                                 Score 31; DB
Pred. No. 44;
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                                                                                                                                                                                                                                                                                                DB 2; Length 260;
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A:Molecule type: DNA
A:Residues: 1-1460 <BOWS
A:Residues: 1-1460 <BOWS
A:Residues: GR Z47647, EMBC 2381,5 MID y603997, FTD.y763231, MIDS.YIEllSc P.Gorsch, L C : Dockendorff, T C ; Cole. C.N.
J. Cell Biol. 129, 934-9545, 1995
A:Title: A conditional allele of the social repeat-containing yeast nucleoporin PAT7
A:Reference number: A57285; MUID:955283676: PMID:77444666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
S48457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C)Function:
A Description insolear pare complex protein involved in mRNA export C;Keywords: nucleus
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C:Date: 13-Sep-1996 #sequence_revision (:-Sep-1996 #text_change 31-Jan-1997
C:Accession: 151225
                                                                                             phosphotransferase system enzyme II, ga actitul specific, protein A : Esche C:Species: Escherichia coli A:Variety: strain EG3132
C:Date: 28-Oct:1995 *sequence_revision = C-Now-luga *Fext_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: DNA
A:Residues: 1-1101, T, 1103-1460 <00P:
A:Cross-references: GB:L40634
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subsited to the EMET 1949 [[trary]
A:Reference number: $48455
A:Accession: $48457
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K.Alturnate names: protein YIL115c
C.St. Nice cooking -
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                   R:Nobelmann, B.; Lengeler, J.W.
Biochim. Biophys. Acta 1262, 69-72, 1995
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A; Residues: 1-263 <THI>
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A;Status: preliminary; translated from GH/EMBL/DDBJ
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A;Reference number: I51225; MUID-94139577, PMID-9308883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Thisse, C.; Thisse, B.; Schilling, T.F., Postlethwait, J.H. Development 119, 1203-1215, 1993
A; Title: Sequence of the gat operon for galactitol utilization from
                                                                    C; Accession: $55903; $49081
                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
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Pare: Object 1994 #sequency_posision
Accession: 8484s; Asize85
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Best Local Similarity
Matches 5; Conserv
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71.48;
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71.4%;
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Pred. No. 2.6e+(2)
2: Mismatches (
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2; Mismatches (
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137 LKEYFT 142

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IA Res. 8, 11-22, 2001
Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genometric number: A99629; MUID:21156231; PMID:11288796
Accession: A90991
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Residues: 1-150 ≺NCB→
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s system, Julactitol-specific IIA component - Escherichia coli (strain 0157:H7, substr
Species: Escherichia coli
Date: 18-Jul-2001 *sequence_revision 18-Jul-2001 *text_change 27-Mow 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:AE000298; GB-0000096; NID:g1786395; FIDN:AAC75155.1; FID:g1788410.
Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Rose, D.J.; Mau, B.; Shao, Y.
lence 277, 1453-1462, 1997
Title: The complete genome sequence of Escherichia coli K-12
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Accession: E64976
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Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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                                                                                                                                                                                                  Cross-references: GB:BA000007; PIDN:BAB36320.1; PID:gl3362366; GSPDB:GN00154
Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, sawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A90991
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                                                                                                                                                        Gene: ECs2897
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Residues: 1-150 <HAY>
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galactitol-specific IIA component - Escherichia coli (strain K-12)
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                                                                Conservative
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    Mismatches

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Fred. No. 41:
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Pred. No.
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Pred. No. 41;
                                                                  1; Mismatches
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RESULT 15
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A;Experimental source: strain O157:H7, sobstrain EDL933
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    NyAlternate names: aspartate transcarbonoylase C;Species: Triticum aestivum (common wheat) C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999 C;Accession: S47625 R;Bartlett, T.J.; Albangbee, A.; Bruce, I.J.; Donovan, P.J.; Yon, R.J. Biochim. Biochim. Biochim. Biochim. 187-193, 1994 A;Reference number: S47625; MUID:94355374; PMID:8075153 A;Accession: S47625; MUID:94355374; PMID:8075153
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A; Residues: 1-150 <STO>
A; Cross-references GB./
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A;Accession: C85836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                              A:Experimental source: var. Avalon C:Superfamily, ornithine carbamoyltrans(crase: aspartate/ornithine carbamoyltrans(crase: homotrimer C:Keywords: pyrimidine nucleotide biosynthesis: transferase: homotrimer F:1-223/Comain. aspartate/ornithine carbamoyltransferase homology (fraument) <ACI >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aspartate carbamoyltransferase (EC 2.1.3.2) - wheat (fragment)
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: Davis, N.W.: (im, A.: Dimalanta, E.: Potamousis: K.: A)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

esult No	Score	Match YastQ	Query Match Length DB	ਬੁਰ	ID	Description
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15	27	75.0	3.2	10	US-09-144-838-14	Sequence 14, Appl
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17	27	75.0	درد	10	US-09-144-838-15	15,
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1 27 75.0 68 9 US-09-742-793A-29 12 27 75.0 68 10 US-09-744-638-10 12 27 75.0 68 10 US-09-744-838-10 12 27 75.0 68 10 US-09-144-838-34 12 27 75.0 68 10 US-09-144-838-34 12 27 75.0 68 10 US-09-144-838-43 12 27 75.0 69 10 US-09-144-838-44 12 27 75.0 69 10 US-09-144-838-44 12 27 75.0 69 10 US-09-144-838-44 12 28 28 28 28 28 28 28 28 28 28 28 28 28	### 27 75.0 89 10 05-09 734-77-8 ### 27 75.0 91 8 05-09-72-939-21 S ### 27 75.0 91 9 05-10
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31 27 75.0 68 9 US-09-742-793A-29 32 27 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-45 47 75.0 69 10 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-45 41 27 75.0 91 9 US-09-144-838-45 42 27 75.0 91 9 US-09-144-838-45 43 27 75.0 91 9 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-45 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45	TATAL TABLE OF THE PROPERTY OF
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31 27 75.0 68 9 US-09-742-794A-29 32 77 75.0 68 10 US-09-144-828-10 34 27 75.0 68 10 US-09-144-828-10 34 27 75.0 68 10 US-09-144-828-10 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 37 27 75.0 68 10 US-09-144-838-42 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-45 41 27 75.0 68 10 US-09-144-838-45 42 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 45 27 75.0 69 10 US-09-144-838-45 47 75.0 91 9 US-09-144-77-8 48 US-08-7-2-939-21 49 US-10-17-275-8	PARTICLE 4.4 OF LOWERS SAND ACTOR FARET W USCLULDENT NO. APPLICANT. POTSYTH, P. Allyn APPLICANT. Dilsen, Kari L. APPLICANT. Dilsen, Kari L. APPLICANT: Dyskind, Judith W. TILLE OF INVENTION. Genes identified as required TILLE OF INVENTION. FRUITSTATE 1000 TOTHER APPLICATION. FRUITS AND ACTOR APPLICATION ARMED 98 13 13 469 COMPENI APPLICATION NOMBER. 2004-12-19 FRIOR APPLICATION NOMBER. 28 66/37/005 PRIOR BILLING PARE. 1049-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 27 75.0 68 10 US-09-144-638-10 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 46 27 75.0 69 10 US-09-144-838-44 47 27 75.0 69 10 US-09-154-477-8 48 10 US-09-144-838-44 49 27 75.0 91 9 US-09-27-39-21 49 US-09-27-275-8 40 27 75.0 91 9 US-09-27-275-8 41 27 75.0 91 9 US-09-27-275-8 42 43 44 45 45 45 45 45 45 45 45 45 45 45 45	FARMET W. USING 1.22718A1 REMERAL INFORMATION: APPLICANT: PORSYTH P. Allyn APPLICANT: Dilsen, Kari L. APPLICANT: Zyskind, Judith W. 111LE OF INVENTION: Genes identified as required TITLE OF INVENTION: FULL FARMER 18: 15 voli FILE APPLICATION NUMBER: 18: 17.74 ves PRIOR APPLICATION NUMBER: 38: 66/177075 PRIOR APPLICATION NUMBER: 38: 66/177075 PRIOR APPLICATION NUMBER: 38: 66/177075 PRIOR BILLING PATE: 1949-12-23 NUMBER OF SEU ID NOS: 481
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31 27 75.0 68 9 US-09-742-734-29 3 31 27 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-164-838-10 34 27 75.0 68 10 US-09-164-838-34 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-45 44 42 27 75.0 69 10 US-09-144-838-45 44 43 27 75.0 69 10 US-09-144-838-45 44 42 27 75.0 69 10 US-09-144-838-45 44 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 9 US-09-144-838-45 46 27 75.0 9 US-09-144-838-45 46 2	APPLICABLE Objects Agrilled Applicable Objects Objec
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31 27 75.0 68 9 US-09-742-794A-29 32 27 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-45 37 27 75.0 68 10 US-09-144-838-45 38 27 75.0 68 10 US-09-144-838-45 39 27 75.0 68 10 US-09-144-838-45 40 27 75.0 68 10 US-09-144-838-45 41 27 75.0 69 10 US-09-144-838-45 42 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 91 8 US-09-144-838-45 45 27 75.0 91 8 US-09-144-838-45 47 27 75.0 91 8 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28	APPLICABLE 2988/104, 3041th W. APPLICABLE 2888/104, 3041th W. TITLE OF INVENTION Genes identified a required TITLE APPLICABLE ELLIFA 109A COPPERI APPLICATION MEMBER 38, 73, 74, 669 OTFFERI FILINI (AMF 2004)-12-19 FRIOR APPLICATION NUMBER 38, 66,717,005 PRIOR ELLING PATE 1949-12-23 NUMBER OF SEU ID NOS: 481
31 27 75.0 68 9 US-09-74-754-751-40180 32 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 45 27 75.0 69 10 US-09-144-838-45 46 27 75.0 69 10 US-09-144-838-45 47 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 10 US-09-144-838-	APPLICANT: Zyskind, Judith W.  TITLE OF INVENTION Recess identified as required TITLE OF INVENTION   FULLIFY 1004 S. Soli File RESERBNOW ELLIFA 1009A    COFFERI APPLICATION REMBER 195 N. 74 6.69    COFFERI FILIN LATE   2000-12-19    FRICE APPLICATION NUMBER   US 60/37 0.05    PRIOR APPLICATION NUMBER   2000-12-23    NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 27 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-10 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 68 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 46 27 75.0 69 10 US-09-144-838-44 47 27 75.0 69 10 US-09-144-838-44 48 27 75.0 69 10 US-09-144-838-44 49 10 US-09-144-838-44 40 US-09-144-838-44 40 US-09-144-	APPLICANT: Zyskind, Judith W. TILE DE INVENTION: despes identified by required TITLE DE INVENTION: proliferation of coli ELLE REPERENCE: ELLIFA 009A CUPPERI APPLICATION RUMBER: 25,77,74,765 PRIOR APPLICATION NUMBER: 25,67,770,75 PRIOR APPLICATION NUMBER: 25,67,770,75 PRIOR ELLING PATE: 1940-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734A-29 32 77 75.0 68 10 US-09-64-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 46 27 75.0 69 10 US-09-144-838-44 47 27 75.0 69 10 US-09-144-838-44 48 27 75.0 69 10 US-09-14-838-44 49 27 75.0 69 10 US-09-14-838-44 49 27 75.0 69 10 US-09-14-838-44 40 27 75.0 91 9 US-09-14-838-45 40 27 75.0 91 9 US-09-14-838-45 41 27 75.0 91 9 US-09-14-838-45 42 27 75.0 91 9 US-09-14-838-45 43 27 75.0 91 9 US-09-14-838-45 44 27 75.0 91 9 US-09-14-838-45 45 27 75.0 91 9 US-09-14-838-45 46 27 75.0 91 9 US-09-14-838-45 47 27 75.0 91 9 US-09-14-838-45 48 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 40 27 75.0 91 9 US-09	TITLE OF INVESTION REPORT HOLD IN POPULTAR TO THE TELEVISION PROPERTY OF THE PERFECT OF THE POPULTAR WHEE USING A FEBRUAR FOR THE POPULTAR WHEE USING A PELLOATION NUMBER USING A SECURIOR OF SECURIORS: 481
31 27 75.0 68 9 US-09-742-734-29 32 77 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 69 10 US-09-144-838-45 42 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 44 27 75.0 91 8 US-09-144-838-45 44 27 75.0 91 8 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-45 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 U	TITLE OF INVENTION CROSS Identified as required TITLE OF INVENTION   Exclise Fation of Soli File Repression   Ellifa ones   COMPENT ARELIATION NUMBER   DS   COMPENT ARELIATION NUMBER   DS   COMPENT ARELIATION NUMBER   DS   COMPENT OF STREET   TO A COMPENT OF SECULO ROSS   481
31 27 75.0 68 9 US-09-742-734-29 32 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-10 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-45 46 27 75.0 69 10 US-09-144-838-45 47 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 10 US-09-144-8	TITLE OF INVENTION Repres Identified by required TITLE OF INVENTION   FULL Feat for the voli File Reserver   EULIFA GOAD    FILE RESERVER   EULIFA GOAD   12-11-41   6-69    COFFERI ADELITATION REPRES   12-11-11   6-69    FRICE APPLICATION NUMBER   10-60/17 GOS    PRIOR APPLICATION NUMBER   10-12-23    NUMBER OF SEQ ID NOS:   481
31 27 75.0 68 9 US-09-742-734-29 3 32 27 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-164-838-10 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-43 36 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-45 44 42 27 75.0 91 9 US-09-144-838-45 44 42 27 75.0 91 9 US-09-144-838-45 45 44 45 45 45 45 45 45 45 45 45 45 4	TITLE OF INVESTION FRUIT FATTE OF SOLI FILE REFERENCE: ELLIFA 109A. COPPERI ARCHITATION REMBER 92 10, 74 1 649 COPPERI FILIN (ANE 2000-12-19 EROOR APPLICATION NUMBER: 98 66/37 1075 PROOR PRILING PARTE: 1949-12-23 NUMBER 05 SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 27 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-12 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-14-838-44 43 27 75.0 69 10 US-09-14-838-44 44 27 75.0 69 10 US-09-14-838-44 44 27 75.0 69 10 US-09-14-838-44 45 27 75.0 69 10 US-09-14-838-44 46 27 75.0 69 10 US-09-14-838-44 47 27 75.0 69 10 US-09-14-838-44 48 27 75.0 69 10 US-09-14-838-44 49 27 75.0 69 10 US-09-14-838-44 49 27 75.0 69 10 US-09-14-838-44 40 27 75.0 69 10 US-09-14-838-44 41 27 75.0 69 10 US-09-14-28-38-44 42 27 75.0 69 10 US-09-14-28-38-44 43 27 75.0 69 10 US-09-14-28-38-44 44 27 75.0 91 9 US-09-14-28-38-44 45 27 75.0 91 9 US-09-14-238-43 46 27 75.0 91 9 US-09-14-238-43 47 27 75.0 91 9 US-09-14-238-43 48 27 75.0 91 9 US-09-14-238-44 49 27 75.0 91 9 US-09-14-28-38-44 49 27 75.0 91 9 US-09-14-28-48-48-48-48-48-48-48-48-48-48-48-48-48	TITLE OF INVENTION   FOLISHMENT OF SOII FILE RESERVED   ELLIFA ADAR COMPRENT APPLICATION NUMBER   DS [0] 74 669 PUSERNI FILIN (ASE 2000-12-19) FRIOR APPLICATION NUMBER   DS 66/370075 PRIOR APPLICATION NUMBER   DS 66/370075 PRIOR PILING PATE   1940-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-794A-29 32 27 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-14-838-44 44 27 75.0 69 10 US-09-14-838-44 45 27 75.0 69 10 US-09-14-838-45 46 27 75.0 91 9 US-09-14-838-45 47 27 75.0 91 9 US-09-14-838-45 48 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 40 27 75.0 91 9 US-09-14-838-45 41 27 75.0 91 9 US-09-14-838-45 42 27 75.0 91 9 US-09-14-838-45 43 27 75.0 91 9 US-09-14-838-45 44 27 75.0 91 9 US-09-14-838-45 45 27 75.0 91 9 US-09-14-838-45 46 27 75.0 91 9 US-09-14-838-45 47 27 75.0 91 9 US-09-14-838-45 48 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 40 27 75.0 91 9 US-09-14-838-45 41 27 75.0 91 9 US-09-14-838-45 42 27 75.0 91 9 US-09-14-838-45 43 27 75.0 91 9 US-09-14-838-45 44 27 75.0 91 9 US-09-14-838-45 45 27 75.0 91 9 US-09-14-838-45 46 27 27 27 27 27 27 27 27 27 27 27 27 27	TITLE OF INVENTION   FOLISCEPHS of the FEDERAL REPERSENCE   ELLIFACIONA   COPPERS   APPLICATION NUMBER   DS [0] 74 C49   COPPERS   APPLICATION NUMBER   DS [0] 75 C75   ERICH APPLICATION NUMBER   DS [0] 77 C75   PPIOP   FILING DATE   1049-12-23   NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734-29 32 77 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-164-898-10 34 27 75.0 68 10 US-09-144-898-12 35 27 75.0 68 10 US-09-144-898-32 35 27 75.0 68 10 US-09-144-898-43 36 27 75.0 68 10 US-09-144-898-43 37 75.0 68 10 US-09-144-898-43 38 27 75.0 68 10 US-09-144-898-43 39 27 75.0 68 10 US-09-144-898-43 40 27 75.0 68 10 US-09-144-898-43 41 27 75.0 69 10 US-09-144-898-44 42 27 75.0 69 10 US-09-144-898-44 43 27 75.0 69 10 US-09-144-898-44 44 27 75.0 91 8 10 US-09-144-898-44 45 27 75.0 91 9 US-09-144-898-45 44 27 75.0 91 9 US-09-144-898-45 45 27 75.0 91 9 US-09-14-898-45 47 27 75.0 91 9 US-09-14-898-45 48 27 75.0 91 9 US-09-14-898-45 49 27 75.0 91 9 US-09-14-898-45 40 27 27 27 27 27 27 27 27 27 27 27 27 27	FILE REFERENCE. ELLIFA 1094 CUFFERI APPLICATION NUMBER 18,70,74 689 CUFFERI FILINI DATE 2003-12-19 FRICE APPLICATION NUMBER 18,70,74 0.5 PRICE APPLICATION NUMBER. 18,60,717/0.05 PRICE FILING DATE 1049-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734.29 32 27 75.0 68 10 US-09-164-761-40180 33 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-12 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 89 10 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-45 47 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 27 27 27 27 27 27 27 27 27 27 27 27	FILE REFERENCE: ELLIFA 100A CUPPERT APPLICATION NUMBER 98.73, 747 669 CUSPERT FILING NAME 2000,12-19 FRICE APPLICATION NUMBER. 98.60/1700.5 PPIOR FILING DATE. 1049-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734-29 32 27 75.0 68 10 US-09-164-61-40180 33 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-43 36 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-44 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 27 27 27 27 27 27 27 27 27 27 27 27	FILE PEPERENCE: ELLIFA 1009A CUMPERT APPLICATION NUMBER: 38,73,747,649 COMPERN FILING NATE: 2000-12-19 FRICE APPLICATION HOMBER: 38,66/37/10/5 PPICE FILING DATE: 1049-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 27 75.0 68 10 US-09-164-61-40180 33 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 46 27 75.0 69 10 US-09-144-838-44 47 27 75.0 69 10 US-09-144-838-44 48 27 75.0 69 10 US-09-144-838-44 49 27 75.0 69 10 US-09-144-838-44 49 27 75.0 69 10 US-09-144-838-44 40 27 75.0 69 10 US-09-144-838-44 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 91 9 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-44 45 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-44 46 27 27 27 8 8 9	FILE REPERENCE: ELLIFA 109A COPPERI APPLICATION RUMBER 125 11 74 66 COMPERI FIZIN (AIE 2000-12-19 PRIOR APPLICATION NUMBER: 08 66/37 1075 PRIOR FILING PATE: 1940-12-23 NUMBER OF SEU ID NOS: 481
31 27 75.0 68 9 US-09-742-794A-29 32 27 75.0 68 10 US-09-164-614-0180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 91 9 US-09-144-838-44 46 27 75.0 91 9 US-09-144-838-45 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 U	CURPENT AREMAN, F. BUTLAR HOMA CURPENT APPLICATION NUMBER 18: [1] 74 66 FORFERT FILLIN (WATE 2000)-12-19 FORE BILLING FATE 1949-12-23 FORFOR BILLING FATE 1949-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-794A-29 32 27 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 69 10 US-09-144-838-45 42 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-45 41 27 75.0 91 9 US-09-144-838-45 42 27 75.0 91 9 US-09-147-838-45 43 27 75.0 91 9 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 47 10 US-09-144-838-45 48 10 US-09-144-838-45 49 10 US-09-144-838-45 40 10 US-09-144-838-4	COPPER APPLICATION REMBER 38 10,74 % 6 COPPER PETCH INTELLET 1000-12-19 ERICK APPLICATION NUMBER 38 66/37 0.05 PRIOR BILLING PATE: 1049-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734-29 32 27 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-838-19 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-45 40 27 75.0 68 10 US-09-144-838-45 40 27 75.0 68 10 US-09-144-838-45 41 27 75.0 68 10 US-09-144-838-45 42 27 75.0 68 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 91 8 US-09-144-838-45 44 27 75.0 91 8 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 47 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-45 41 27 75.0 91 9 US-09-144-838-45 42 27 75.0 91 9 US-09-144-838-45 43 27 75.0 91 9 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-45 41 27 75.0 91 9 US-09-144-838-45 42 27 75.0 91 9 US-09-144-838-45 43 27 75.0 91 9 US-09-144-838-45 44 27 27 27 27 27 27 27 27 27 27 27 27 27	COPPERT ADELLIATION RUMBER 18, 10, 74, 66 CHEFENT FILEN TATE 2000-12-19 ERICR APPLICATION NUMBER 10, 66,7770-05 PRICR FILING PATE 1094-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 27 75.0 68 10 US-09-164-761-40180 33 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-12 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-43 44 27 75.0 69 10 US-09-144-838-43 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-43 47 75.0 91 9 US-09-144-838-43 48 27 75.0 91 9 US-09-144-838-44 49 27 75.0 91 9 US-09-144-838-45 49 10 US-09-14	CTEPENT APPLICATION NUMBER 18 10 74 66 PERSON FILLIN [MIE 2000-12-19] FRIOR APPLICATION NUMBER 08 66/37 00 56 PRIOR FILLING DATE 1044-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 77 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-45 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 US-09-144-838-45 49 US-09-144-838-45 49 US-09-144-838-45 49 US-09-144-838-45 49 US-09-144-838-45 40 US-09-144-838-45 40 US-09-144-838-45 40 US-09-144-838-43	PRICE APELIATION HOMBER 18, 14 70 PERCE APELICATION NUMBER 198 60/17 0075 PRICE FILING PATE 1949-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 27 75.0 68 10 US-09-164-761-40180 34 27 75.0 68 10 US-09-144-848-10 34 27 75.0 68 10 US-09-144-848-10 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 46 27 75.0 69 10 US-09-144-838-45 47 27 75.0 69 10 US-09-144-838-44 48 27 75.0 69 10 US-09-144-838-45 49 27 75.0 69 10 US-09-144-838-45 40 27 75.0 91 9 US-09-14-838-45 44 27 75.0 91 9 US-09-14-838-45 45 27 75.0 91 9 US-09-14-27-8 46 10 US-09-144-838-45 47 10 US-09-144-838-45 48 10 US-09-144-838-45 49 10 US-09-144-838-45 49 10 US-09-144-838-45 49 10 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-45 40 27 75.0	PERENT FIZIN (AIF 200)-12-19 FROR APPLICATION NUMBER. US 66/37/0/5 PROF FILING PATE 1940-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734A-29 32 77 75.0 68 10 US-09-64-761-40180 34 27 75.0 68 10 US-09-144-848-10 34 27 75.0 68 10 US-09-144-848-10 34 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-43 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 69 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 91 9 US-09-144-838-43 46 27 75.0 91 9 US-09-144-838-44 47 27 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 75.0 91 9 US-09-14-838-45 40 27 75.0 91 9 US-09-14-838-45 41 27 75.0 91 9 US-09-14-838-45 42 27 75.0 91 9 US-09-14-838-45 43 27 75.0 91 9 US-09-14-838-45 44 27 75.0 91 9 US-09-14-838-45 45 27 75.0 91 9 US-09-14-838-45 46 27 75.0 91 9 US-09-14-838-45 47 27 75.0 91 9 US-09-14-838-45 48 27 75.0 91 9 US-09-14-838-45 48 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 49 27 75.0 91 9 US-09-14-838-45 40 27 75.0 91 9 US-09-14-838	**************************************
31 27 75.0 68 9 US-09-7%2-794A-29 32 77 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-844-848-10 34 27 75.0 68 10 US-09-444-848-10 34 27 75.0 68 10 US-09-444-838-34 35 27 75.0 68 10 US-09-444-838-43 36 27 75.0 68 10 US-09-444-838-43 37 27 75.0 68 10 US-09-444-838-43 38 27 75.0 68 10 US-09-444-838-43 40 27 75.0 68 10 US-09-444-838-43 41 27 75.0 68 10 US-09-44-838-44 42 27 75.0 69 10 US-09-44-838-44 43 27 75.0 69 10 US-09-44-838-45 44 27 75.0 69 10 US-09-44-838-45 44 27 75.0 91 9 US-09-44-838-45 45 27 75.0 91 9 US-09-44-838-45 46 27 75.0 91 9 US-09-44-838-45 47 27 75.0 91 9 US-09-44-838-45 48 27 75.0 91 9 US-09-44-838-45 49 27 75.0 91 9 US-09-44-838-45 49 27 75.0 91 9 US-09-44-838-45 40 27 75.0 91 9 US-09-44-838-45 41 27 75.0 91 9 US-09-44-838-45 42 27 75.0 91 9 US-09-44-838-45 43 27 75.0 91 9 US-09-44-838-45 44 27 75.0 91 9 US-09-44-838-45 44 27 75.0 91 9 US-09-44-838-45 45 27 75.0 91 9 US-09-44-838-45 46 27 75.0 91 9 US-09-44-838-45 47 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	""FRENT FILIN' (ATE 2"00-12-19) FRICE APPLICATION NUMBER. US 66/17/00 PRICE FILING DATE: 1999-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 77 75.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-898-10 34 27 75.0 68 10 US-09-144-898-12 35 27 75.0 68 10 US-09-144-898-34 35 27 75.0 68 10 US-09-144-898-43 36 27 75.0 68 10 US-09-144-898-43 37 27 75.0 68 10 US-09-144-898-43 38 27 75.0 68 10 US-09-144-898-43 40 27 75.0 68 10 US-09-144-898-43 41 27 75.0 69 10 US-09-144-898-44 42 27 75.0 69 10 US-09-144-898-45 43 27 75.0 69 10 US-09-144-898-45 44 27 75.0 91 8 US-09-144-898-45 44 27 75.0 91 9 US-09-144-898-43 45 27 75.0 91 9 US-09-144-898-45 47 27 75.0 91 9 US-09-144-898-45 48 27 75.0 91 9 US-09-144-898-45 49 27 75.0 91 9 US-09-144-898-45 40 27 75.0 91 9 U	CTREEN FILIN: DATE 200-12-19 FRICE APPLICATION NUMBER: US 66/37/00 PRICE FILING DATE: 1040-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-7%2-794A-29 32 77.0 68 10 US-09-864-761-40180 34 27 75.0 68 10 US-09-144-898-10 34 27 75.0 68 10 US-09-144-898-12 35 27 75.0 68 10 US-09-144-898-34 35 27 75.0 68 10 US-09-144-898-43 37 27 75.0 68 10 US-09-144-898-43 38 27 75.0 68 10 US-09-144-898-43 39 27 75.0 68 10 US-09-144-898-43 40 27 75.0 68 10 US-09-144-898-45 41 27 75.0 69 10 US-09-144-898-45 42 27 75.0 69 10 US-09-144-898-45 43 27 75.0 69 10 US-09-144-898-45 44 27 75.0 69 10 US-09-144-898-45 43 27 75.0 91 9 US-09-144-898-45 44 27 75.0 91 9 US-09-144-898-45 44 27 75.0 91 9 US-09-144-898-45 45 27 75.0 91 9 US-09-144-898-45 46 27 75.0 91 9 US-09-144-898-45 47 27 75.0 91 9 US-09-144-898-45 48 27 75.0 91 9 US-09-144-898-45 49 27 75.0 91 9 US-09-144-898-45 49 27 75.0 91 9 US-09-144-898-45 40 27 75.0 91 9 US-09-144-898-45 41 27 75.0 91 9 US-09-144-898-45 42 27 75.0 91 9 US-09-144-898-45 43 27 75.0 91 9 US-09-144-898-45 44 27 75.0 91 9 US-09-144-898-45 45 27 75.0 91 9 US-09-144-898-45 46 27 PS-09-144-898-45 47 27 27 27 27 27 27 27 27 27 27 27 27 27	PREMI FLIEN INTE A 100712719 FRICE APPLICATION HOMBER. US 60/37/0/3 PRICE FILING DATE: 1040-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-74-754-29 32 27 75.0 68 10 US-09-164-6761-40180 33 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-12 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-34 36 27 75.0 68 10 US-09-144-838-42 38 27 75.0 68 10 US-09-144-838-43 39 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-44 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-45 44 27 75.0 69 10 US-09-144-838-45 45 27 75.0 69 10 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-45 47 75.0 91 9 US-09-144-838-45 48 27 75.0 91 9 US-09-144-838-45 49 27 27 27 8 8 9	FRICE APPLICATION NUMBER: 08-66/37/00 PRICE SPLICATION TOWNS 1949-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-742-734-29 32 27 75.0 68 10 US-09-164-61-40180 34 27 75.0 68 10 US-09-144-838-10 34 27 75.0 68 10 US-09-144-838-12 35 27 75.0 68 10 US-09-144-838-34 35 27 75.0 68 10 US-09-144-838-43 36 27 75.0 68 10 US-09-144-838-43 37 27 75.0 68 10 US-09-144-838-43 38 27 75.0 68 10 US-09-144-838-43 40 27 75.0 68 10 US-09-144-838-43 41 27 75.0 68 10 US-09-144-838-44 42 27 75.0 69 10 US-09-144-838-44 43 27 75.0 69 10 US-09-144-838-44 44 27 75.0 69 10 US-09-144-838-44 45 27 75.0 69 10 US-09-144-838-44 46 27 75.0 69 10 US-09-144-838-44 47 27 75.0 69 10 US-09-144-838-44 48 27 75.0 69 10 US-09-144-838-44 49 27 75.0 69 10 US-09-144-838-45 40 27 75.0 91 9 US-09-144-838-44 41 27 75.0 91 9 US-09-144-838-45 42 27 75.0 91 9 US-09-144-838-45 43 27 75.0 91 9 US-09-144-838-45 44 27 75.0 91 9 US-09-144-838-45 45 27 75.0 91 9 US-09-144-838-45 46 27 75.0 91 9 US-09-144-838-45 47 11 E-FERMATICH PARTIES TO STANDENTS APPLICANT: POTS: No. 112, 1274: 59 APPLICANT: Dalsen, Karl L. APPLICANT: Zyskind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: E-FERMATICH PARTIES TO STANDENTS ALLIFAN UNMBER 1987-1987-1987-1991 APPLICANT: E-FERMATICH PARTIES TO STANDENTS ALLIFAN UNMBER 1987-1987-1987-1991 APPLICANT: E-FERMATICH PARTIES TO STANDENTS ALLIFAN UNMBER 1987-1987-1987-1991 APPLICANT: E-FERMATICH PARTIES TO STANDENTS ALLIFAN UNMBER 1987-1987-1991 APPLICANT: E-FERMATICH PARTIES TO STANDENTS ALLIFAN UNMBER 1987-1987-1991 APPLICANT: E-FERMATICH PARTIES TO STANDENTS ALLIFAN UNMBER 1987-1987-1987-1991 ALLIFAN UNMBER 1987-1987-1987-1991 ALLIFAN UNMBER 1987-1987-1991 ALLIFAN UNMBER 1987-1991 ALLIFAN U	ERICE APPLICATION HOMBER. US 60/37/00 PPIOE FILING DATE: 1999-12-23 NUMBER OF SEQ ID NOS: 481
31 27 75.0 68 9 US-09-74-754-29 32 27 75.0 68 10 US-09-164-61-40180 34 27 75.0 68 10 US-09-144-88-10 34 27 75.0 68 10 US-09-144-88-10 35 27 75.0 68 10 US-09-144-83-34 36 27 75.0 68 10 US-09-144-83-43 37 75.0 68 10 US-09-144-83-43 38 27 75.0 68 10 US-09-144-83-43 39 27 75.0 68 10 US-09-144-83-43 40 27 75.0 68 10 US-09-144-83-43 41 27 75.0 69 10 US-09-144-83-44 42 27 75.0 69 10 US-09-144-83-44 43 27 75.0 69 10 US-09-144-83-43 44 27 75.0 69 10 US-09-144-83-43 45 27 75.0 69 10 US-09-144-83-43 46 27 75.0 69 10 US-09-144-83-43 47 27 75.0 69 10 US-09-144-83-43 48 27 75.0 69 10 US-09-144-83-43 49 27 75.0 91 9 US-09-144-83-43 49 27 75.0 91 9 US-09-144-83-43 49 27 75.0 91 9 US-09-144-83-43 45 27 27 27 27 27 27 27 27 27 27 27 27 27	ERIOR APPLICATION NUMBER: US 60/37 000 ppiop filing pate: 1944-12-23 NUMBER OF SEQ ID NOS: 481
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RESULT 1

RESULT 1

REPART 24.4 Apt Librica 12/10741/59

Farmer 24.4 Apt Librica 12/10741/59

Farmer 27 TEXTURE 2778A1

REPRITANT Dilsen, Kari L.

APPLICANT PROSYTH, P. Allyn

APPLICANT DISSEN, Kari L.

COMPANI DISSENTANT DISSENTANT DISSENTANT PROPERTY APPLICANT NUMBER DISSENTED 10 NOTE 11 NOTE
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PRIOR FILING DATE: 200-12-7
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 50/257,331
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12610
LENGTH: 5795
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Patent No. US20020061569Al
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Best Local Similarity 83.3%;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: NUCLEI 07H
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/207.727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
DRIOR ETTENS OF THE PRIOR APPLICATION NUMBER: 60/253,625
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ITILE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
GURPENT APPLICATION NUMBER 19:00.01:1242
CUPPENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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                     PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                      PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                   PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus 09-815-242-12610
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
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                                                2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05/09/815,242

    Mismatches

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Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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; TYPE: PRT; ORGANISM: Helicobacter pylori
US-09-815-242-11289
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CORPENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
FEITE APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                               US-09-782-874-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 11289
                                                         Sequence 3, Application US/09782874 Patent No. US20010023067A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11471
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APPLICANT:
APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE PEFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                     APPLICANT: Wassenegger, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T.
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Riedel, Leonhard
Schiebel, Winfrie
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                                                                                                                                                                                                                                                                                                                          77 8%; Score 2H; DB 10; 100.0%; -Fred. No. 1.4e+0
Winfried
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JS-09-782-874-3
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JS-09-912-020-350
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REGISTRATION NUMBER: 27,794
REFERENCE/GOOKET NUMBER: MPS-1
TELECOMMUNICATION INFORMATION.
TELEPHONE: 212-596-9000
TELEPAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 3.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 350, Application US/20412020 Patent No. US20020045592A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarit;
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Kari L
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamle M.
                 PMIOR APPLICATION NUMBER: 04,442,704 PRIOR FILING DATE: 2200-01-27 PRIOR APPLICATION NUMBER: 60,7117,405 PRIOR FILING DATE: 1999-01-27 NUMBER: OF SEO ID NOS: 485
                                                                                                                                 APPLICANT: XU, H. HOWARD
TITLE OF INVENTION, GENES TUFNITHED AS REQUIRED FOR FROITERRATION IN
TITLE OF INVENTION SECHERICHIA COLI
FILE REFERENCE: ECHIPA DOLDAY
CURPENT APPLICATION HOMBER 75.75, 311.036
CURRENT FILING DATE: 2001 07.23
SUFTWARE: FastSED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 VEEYFIN 150
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBERS US 08/811 583 FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFF: TAIT-N NUMBER US TO FILING DATE: 08-E0b-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                  Carr, Grant J.
                                                                                                                                                                                                                                                                            Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 10; Length 218; Field, NJ. 2.1e+32; Indels 3; Indels
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RESULT 8
US-04-910-430-27
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Best Local Similarity
Whiches 5; Conserve
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// TYPE: PRT
// ORGANISM: E. Coli
US-09-912-020-350
                  SOFTWARE: FASISEO for Windows Versi at 3.0 SEQ ID NO 27 LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application 05/09910430 Patent No. 0520020127235Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 16
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                                                                          CURRENT AFFLICATION MINNER OS,03,910,4
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: COT/FECO, 706
FS.GF HIGHS CATE 1250-30-06
PRIOR APPLICATION NUMBER: GB 9913427 6
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-12-27

PPIOR APPLICATION NUMBER: 09/594,185

PRIOR FILLING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: EP 96115540.5

PRIOR FILLING DATE: 1096-09-27

NUMBER OF SEQ ID NOS: 23

SOFTWARF: Patentin Ver 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Furuichi, Yasuhiro
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITLE OF INVENTION: HIGHIN BIOSYNTHFILD GENES
FILE REFERENCE: Biotin Genes
FILE REFERENCE: Biotin Genes
FILE APPLICATION NUMBER 185,10,031,078
                                                                                                                                                                                                                         APPLICANT: Bollen, Alex
APPLICANT: Leboulle, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MCLECULAR CHARACERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIV
TITLE OF INVENTION: GLANDS
FILE REFERENCE: VANNA229.001CPT
FILE REFERENCE: VANNA229.001CPT
                                                                                                                                                                                                                                                                                                                    APPLICANT: Godfroi, Edmond
APPLICANT: Bollen, Alex
APPLICANT: Leboulle, Gerarc
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 VREFFTS 220
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                                                                                                                                                                                                                                                                                PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
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83.3%;
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57.1%;
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Pred No. 2.7e+02;
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Pred. No. 2.3e+02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10: Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 276;
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CUMPENT APPLICATION NUMBER: US/00/738,626
CURRENT FILING DAIE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DAIE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PET ORGANISM: Drosophila melanogaster 3-10-081-816-5
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3-09-738-626-5605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application Us/19981816
Publication No. US20030045472A1
GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5606. Application US/09738626 Publication No. US20020197605A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION. Chemosensory Sene Family Encoding Sustatory And Olfactory Except TITLE OF INVENTION: Uses Thereof FILE REFERENCE 0.575.640164-A.7TM.AEM CURRENT APPLICATION NUMBER: 05.710.7081.816 CURRENT FILING DATE: 2002-22-22 PRIOR APPLICATION NUMBER: 602-22 PRIOR APPLICATION NUMBER: 602-22 PRIOR APPLICATION NUMBER: 602-23 NUMBER 05 SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-081-816-5
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                                      SOFTWARE: PatentIn ver.
SEQ ID NO 5606
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Axel, Richard APPLICANT: Scott, Krist:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYNUCLECTIBES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                              NUMBER OF SEQ ID NOS: 7059
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TYPE: PRT
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                    LENGTH: 511
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SENOH, AKIHIRO
IKEDA, MASATO
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88;
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Fred. No. 4.1e+62,
1: Mismatches (
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Query Match
Best Local Similarity
Tenhas 5: Conserve
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                                                                                                                                                                                                                     RESULT 12
US-09-770-940-2
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                                                                                                                                                       ; GENERAL INFORMATION:
                                                                                                                                                                         Sequence 2, Application US/09770940 Patent No. US20020009790Al
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Extent No. 0820020061569A1
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CORRENT FILING DATE: 2001-03-21
PRIOP APPLICATION NUMBER: 60/191/078
PRIOP FILING DATE: 2000-03-21
PRIOP APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
FELCE AFFLICATION NUMBER: 60/207.727
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APPLICANT: Kreiberg, J. APPLICANT: Buchholt, H. APPLICANT: Buchholt, H. TITLE OF INVENTION: PROCESS FOR STAFFLIZING PROTEINS IN AN TITLE OF INVENTION: ACIDIC ENVIRONMENT WITH A HIGH-ESTER PECTIN FILE REFERENCE: DYOU14.001APC
                                                                                                        APPLICANT: Christensen, T. APPLICANT: Thorsoe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR EMPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/269,308
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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APPLICANT:
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Xu, H. Howard
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83.3%;
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Pred. No 4.8e+02:
1: Mismatches (
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RESULT 14
JS-09-782-874-2
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ORGANISM: Pseudomonas aeruginosa
IS-09-815-242-5093
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18-09-815-242-5093
Sequence 5093 Application US/MA815242
Patent No. US20020061569A1
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LENGIH: 584
Sequence 2. Application US/09782874
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Best Local Similarity 57.1%;
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PRIOR APPLICATION NUMBER - 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60,257,931
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60,242.578
PRIOR FILING DATE: 2000-10-23
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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Local Similarity 83.3%; Pred. No. 5.4e+02;
hes 5; Conservative 1; Mismatches 0
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Xu, H. Howard
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Pred: No. 6.6e+02;
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Best Local Similarity 57.8
Matches 4, Conservative
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SEQ ID NO 14
LENCTH: 32
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                               APPLICANT: Siani, Michael A. APPLICANT: Wilken, Jill APPLICANT: Simon, Reyna APPLICANT: Simon, Reyna APPLICANT: Kent, Stephen B.H. TITLE OF INVENTION: Modular Protein Sibraries and Methods of Preparation FILE PEFERNTE: 5FFN-020/01US
                                                               EARLIER APPLICATION NUMBER: US EARLIER FILING DATE: 1997-09-04 NUMBER OF SEQ ID NOS: 54
                                                                                                                                     CURRENT APPLICATION NUMBER, US/
CURRENT FILING DATE: 1998-08-31
                                                SOFTWARE: Patentin Ver.
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TELECOMMONICATION INFORMATION
TELEPHONE: 212-596-9000
TELEPAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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TYPE: PRI
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
-09-144-838-14

Query Match
Fest Local Similarity 100.0%: Score 27; DB 10; Length 32;
Hest Local Similarity 100.0%: Pred. No. 55;
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Copyright (c) 1993 - 2003 Compugen Did
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FY SEDITENCE OF 26-99.  RC TISSUE-OSTEOGRAFGS PIRMED=16  RX MEDINF-0230RAFGS PIRMED=16  RX MEDINF-0230RAFGS PIRMED=16  RT "Structural and functional  RT monocyte chemotactic protei  RT chemokine family.";  PL J. Exp Med. 176:59-65(1992  RN [5]  RP SUGUNIT.  RF SUGUNIT.  RF SUGUNIT.  RF SUGUNIT.  RF SUGUNIT.  RT "Structural characterizatio  RT chemoattractant protein-3.  RT chemoattractant protein-3.  RT FIRS Lott. 395:277-282(1996)  CC -!- FUNCTION- CHEMOTACTIC				# # # # # # # # # # # # # # # # # # #
13466; Pnaerts T.P. identification ns (MCP-2 and ).  98111; Park Fowls I m of a monome; ).  ACTOR THAT AT	TANT GLM 69.  70881;  Nomiyama H., Applehaker: cl Optobaker: cl Optobake	IANT GIN-69 19400: omlyama H., ; 8): clouing to the PC c	PRT; 99 A ed) sequence update sequence (CCL colored CCL colored CC	99 1 SY98_SOVIN 104 1 Y376_MYYGE 104 1 Y376_MYYGE 142 1 YE446_STRVY 0 229 1 YE446_STRVY 0 237 1 Y4MC_PHYN 0 237 1 Y4MC_PHYN 0 238 1 RMM_ASTGA 0 244 1 TF4_SCHO 0 246 1 YCSO_BMASU 0 247 1 YE95_SYHYO 0 256 1 TAM_PHILO 0 256 1 TAM_PHILO 0 270 1 PPE1_MAUSE 0 270 1 PPE1_MAUSE
desapper G.: f two human, tumor-derived p-3) belonging to the syves B.D.; chemokine: monocyte	diura R., Fiten P., NA cloning and regulated () (0(1997). Peinherz E.L.: feron-inducible dene in te family.";	ki Y., Miura R., Yoshie O., uence analysis, tissuc ine gene contig on	A. ) ) (Monocyte chemotactic st protein 2) (HC14). stephenata: Enteleostomi) Hominidae, Homo.	p49797 rattus norw 009141 hos taurus p47616 mycoplasma p16463 streptococco 006mp2 ranbida qla p8682 rhizobium s p19791 aspergillus 094476 schizosacch p42968 bacillus su 013767 schizosacch 013767 schizosacch 013767 schizosacch 013767 schizosacch 0137655 mus musculu 0137655

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15-JUL-1999 (Rel. 34. Last annotation update)
Small inducible cytokine A8 precursor (CCLR) (Monocyte chemotactic protein 2) (MCF-2) (Monocyte chemoattractant protein 2).
SCYA8 OR MCP2.
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                                                                                                      Hosang K.K., Knoke I.I., Klaudiny Scheit K.K.:
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MEDLINE=95091716; PubMed=7999015;
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InterPro: IPR001811; Chemokine_IL8.
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Y10802: CAA71760.1; ·.
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9DC7976BB9422F2A 0R064,
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doid P.C.,
Smith D.K., Noonan B., Guild B.T., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
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            -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate CoA + 1,2-diacyl-sn-glycerol 3 phosphate: CoA + 1,2-diacyl-sn-glycerol 3 phosphate: -!- PATHWAY: De novo phospholipid (c)osynthesis: second step. -!- SUBCELLULAR LOCATION: Inner nembrane-associated (Potential). -!- SUBCELLULAR LOCATION: Inner nembrane-associated (Potential). -!- SIMILAFITY: RELOWS 10 THE 1-A-11-SN-GLYCEROL-3-PHOSPHATE
                                                                                                                                     "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pyloria": Nature 397:176-180(1999).
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Interior [Reviole27] C2_hemkine_IL8
Interior [Reviole27] Chemekine_IL8
Interior [Reviole27] IL8;
INTERIOR [Reviole27] SMALL_CYTOKINES_**)
Cytokine, Chemotaxis, Signal, Hepario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by pro-profit institutions on long modified and this statement is statement of entitles requires a license agreement (see lor send an email to licenseeisb-sik.ch).
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Bacteria: Proteobacteria: epsilon subdivision: Hel
                                                                                                                                                                                                                                                                                                                                                                                                                                         1-acyl-sn-glycerol-3-phosphate acyl-transferase (E^ 2.3.1.51) (1-AGP
acyltransferase) (1-AGPAT) (Lysoph-sphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: 248480: CAA88371.1; -. HSSP: P51671: 1EOT.
                                                                                                                                                                                          Trust T.J.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                        Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZJN8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLSC_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                      -1- FUNCIION:
                                                                                                                                                                                                                                                                                                                                                                                                          PLSC OR JHP1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last seguench update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONDCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 LESYT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LESYT 5
                                                                                                   EUNCITION: CONVEKTS LYSOPHOSPHALIDIC ACID (LEA) INTO PHOSPHATIDIC ACID BY INCOPPOPATING ACYL MOJETY AT THE 2 POSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-C) (CHEMOKINE CC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAN BIND HEPARIN.
SHEETING OF HOMODINEP: N POUTLIBRIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILAPITY: BELONGS TO THE INTERINE BETA FAMILY (SMALL CYTOKINE
ACYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS-PROT entry is copyright. It is produced through a collaboratic Swiss Institute of Bioinformatics and the EMBL outstat pean Bloinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10903 MW;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMALL INDUCIBLE CYTOKINE A8.
PYRROLLOONE CARROXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparia binding, Inflammatory response BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D3DAAOF7A964CDB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 25; DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tond as Its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Come http://www.isbrsib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                       Helinobacter groups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             025903;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP 1-acyl-sn-glycerol-3-phosphate acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Eleischmann P.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weddman J.M., Fujil C., Bowman C., Watthey L., Wallin E. Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: AE001550: AAD06852.1: --
InterPro: IPR004552: AGF_acyltransferase.
InterPro: IPR002452: Acyltransferase.
Pfam: PF01553: Acyltransferase; 1.
TIGPFAMs: TIGPAN530: AGP_acyltrn: 1.
Phospholipid biosynthesis: Transferase; Acyltransferase;
                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                   This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Burgean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTAH
                                                                                                                                                                                                                                                                                                                       -!- FATHWAY. De novo phospholipid biosynthesis; second step.
-!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
-!- SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-R-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate CoA + 1.2-diaryl-sn-glycerol 3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acyltransferase) (1-AGFAT) (L_{
m Y}sophosphatidic acid acyltransferase)
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SEQUENCE 237 AA; 27188 MW; E1
entities requires a license agreement (see http://www.ish-sib-ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete yenome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 LESYT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                 ACYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR HP1348.
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E10F517D42A1731F CRC64;
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Best Local Similarity
                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlarage A.R., Dougherty B.A., Tomb. T. F., Adams M.D., Reich C.I.,
Overbeek P., Kitkness E.F. Weinstock K.G. Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Pererson J.D., Sadow P.M., Hanna M.C.,
Utterback T.R., Kelley J.M., Pererson J.D., Sadow P.M., Hanna M.C.,
                                                                                                                                                                                                                                                                                                                                                     Chitch M.D., Roberts P.M., Hurst M.A., Paine B.P., Rerndowsky M.,
Klenk H.-P., Fraser C.M., Smith H.D., Whese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic atchaeon, Methanoconcus
fannaschil":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanocaldococcaceae; Methanocaldococcus (CBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000636; AAD08393.1; TIGR; HP1348; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.
                                                                                                                SEQUENCE
                                                                                                                                                                                                                      Q58121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholipid biosynthesis; Transferase; Acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR004552; AGP_acyltrn.
InterPro: IPR002123; Acyltransferase
                                                                                                                                                                             EMBL; U67518; AAB98714.1; -.
                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein MJ0711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y711_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIGRFAMs; TIGR00530; AGP_acyltrn;
                                                                                                                                 TRANSMEN
                                                                                                                                                Hypothetical protein; Transmembrana; Complete proteome
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is everyight It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                  Š~i⊖nç⊖ 273:1058-1073(1996).
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106 LESYT 110
                                                                      Local
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                          1 LESYT 5
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NCE 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01553; Acyltransferase; 1.
                                                                                                                                                                 MJ0711;
                                                        Similarity
5; Conserv
                                                                                                                  322 AA;
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
AA; 27745 MW; 22805D0EB190BBDD CPC64;
                                                                                                                   38631 MW:
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                                                                        100.0%;
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                                                                                                                                 POTENTIAL
                                                                      Scor:
Pred
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                                                                                                                   prs: 164175044F27 CRC64;
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                                                           Mismatches
                                                                        No. 43;
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                                                                                       DR 1: Length 322:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ng W.V. Kennedy S.P. Mahairas G.G., Berquist B., Pan M., Shukla H.D. Lasky S. R. Baliga N.S. Thorsson V. Strenna J. Strukla H.D. Lasky S. R. Baliga N.S. Thorsson V. Strenna J. Strenna J. Strenna J. Berthall J. Dahl T.A. Welti P. Goo Y.A. Leithauser B. Keller K., Cruz R., Danson M.J., Hough D.W. Leelthauser B. Keller K., Cruz R., Danson M.J., Hough D.W. Leelthauser B., Keller K., Cruz R., Danson M.J., Hough D.W. Leelthauser B., Keller K., Cruz R., Danson M.J., Hough D.W. Leelthauser B., Freitas T. Hou S. Pachiels J. Leentis i F. Thors T. Hou S. Leentis F. Leentis i F. Thors T. Hou S. Liang P. Pilley M. Hood L. Dassarma S., Genome sequence of Halobacterium species NRC-1."

Tenomactic T. Acad Sci U.S. A. 37:1276-12181 (2006)

1- FUNCTION: CATALYZES THE 1.3-ALIYLIC KEARKANUEMENI OF THE HOMALUTIC SURSTRATE ISOPENIENVE (IPP) TO ITS ALIYLIC ISOMEP, DIMETHYLALIXI DEPOSPHATE (DMAPP) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: AF016485; AAC82844.1; ALT_INIT. EMBL: AF016485; AAC82933.1; ALT_INIT. EMBL: AE005145; AAC320768.1; EMBL: AE005169; AA;21040.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib-ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITME-99063795; PubMed-9847077;
Ng W.V., Clufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faus Hall B., Ioratz C., Seto T., Slagel J., Hood L., DasSarma S., "Snapshot of a large dynamic replies of in a halophilic archaeon: megaplasmid or minichromosome?";
Genome Res. 8:1131-1141(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Isopentenyl pyrophosphate isomerase).
(ENII OR VNG5084G OK HO660, AND (ENIZ OR VNG5213G OF H1695) AND
(ENIZ OR VNG6081G) AND (ENI4 OR VNG6445G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9HHE4; 054623;
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                               Isomerase: Isoprene biosynthesis: Flavoprotein; FMN; NADP; Plasmid; Complete proteome.
                                                                                                                                                                                                                                                                                                                     InterPro: IFR603009; FMN_enzyme.
InterPro: IPR000262; FMN_hydx;3e_th
Pfam: PF01070; FMN_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20504483; PubMed-11016950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASMID-PNRC200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacteriaceae: Halobacterium.
NCBI_TaxID=64091:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota, Halobacteria; Halobacteriales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacterium sp. (strain NRC-1).
Plasmid pNRC100, and Plasmid pNRC200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Pel. 40, Last annotation update)
15-0pentenyl diphosphate delta-isomerase (EC 5 3.3 2) (TPP isomerase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N A
                                                                 Local Similarity 100 hes 5: Conservative
1 LESYT 5
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SIMILAKIT: BELOWGS to THE TEP ISOMERASE TYPE 2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
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                                                                                                                                                                                                                    360 AA;
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                                                                                                                                                                                                                    38342 MW; 67814178071D3164 CRC64;
                                                                                                100.0%;
                                                                                                                                       100 08;
                                                             0; Mismatches
                                                                                                        Pred. No. 49;
                                                                                                                                   Score 25; DB 1; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHT;
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Best Local Similarity
Techas 5; Conserve
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Metcalf W.W., Zhang J.K., shi "Muleoni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: 1PR000192; AminotransfV.
PROSITE: PS00595; AA_TRANSFER_CLASS_5: FALSE_NEG.
Serine biosynthesis; Pyridoxine biosynthesis; Transferase.
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                                                                                                                                                                                                                                          ERF1
                                                                                                                                                                                                                                                                                                                    16-007-2001 (Rel. 40, Created)
16-001-2001 (Rel. 40, Last Sequence update)
16-001-2001 (Rel. 40, Last annotation update)
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BINDING 190 190 PYRID VAL EHOSPHATE (BY SIMILARITY)
FELTERE (TO AA. 41544 MW) VIETTO VILETESS44 FRO64;
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                                                       SEQUENCE FROM N.A. PubMed=10844194;
                                                                                                                                          Eukaryota; Diplomonadida; Hexamitidue: Giardiinae: Giardia
NCPI_TaxID~5741;
                                                                                                                                                                                                                                                                                            Eukaryotic peptide chain release factor subunit 1 (eRF1) (Eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NCP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U51905: AAC44430.1; -
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   "Evolution of the eukaryotic transistion termination systems origins
                                                                                                                                                                                                        Giardia lamblia (Giardia intestinalis)
                                                                                                                                                                                                                                                                   release factor 1).
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                              Inagaki Y., Doolittle W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 LESYT 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Yes 100.0%; Pred No. .
100.0%; Pred No. .
100.0%; Milmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 457 AA
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2.6.1.52) (FSAT).
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      RXRG_XENLA
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Best Local Similarity
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Mol. Biol. Evol. 17.982-895(2000).
-:- FUNCTION: Directs the termination of mascent peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-Prol entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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01-0CT-1996 (Rel. 34, Last sequence update)
15-THL-1999 (Pel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                             Blumberg B., Mangelsdort D.J., Dyck J.A., Bitther D.A., Evans R.M., de Robertis E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Amphibia: Batrachia; Amura: Mesobatrachia; Fipeidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa. Chordata: Oraniata: Vertebrata: Euteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RXRG OR NR2B3.
Xenopus laevis (African clawed frog).
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Pfam; PF03464; eRF1_2; 1.
Pfam; PF03465; eRF1_3; 1.
TIGREAMS; TIGROCIOE; eRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR005140: eRF1_1.
InterPro: IPR005141: eRF1_2.
InterPro: IPR005142: eRF1_3.
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InterPro: IPR005140; eRF1_
                                                                                                                                                                                                                    Proc.
                                                                                                                                                                                                                                                           retinoid 'X' receptors and retinoic acid receptors in the Xenopus
                                                                                                                                                                                                                                                                                                                                      MEDLINE-92196110, FubMed-1312717;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae: Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retinoic acid receptor RXR-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RXRG_XENLA
                                                                                                                                                                                                                                                                           "Multiple retinoid-responsive receptors in a single cell: families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 LESYT 34
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TO NATE ACAD. SCI. U.S.A. 89:2321:2325(1992).

FUNTION: INVOLVED IN RETINGE ACID RESPONSE PATHWAY. BINDS
9-CIS RETINGE ACID (9C-RA) (BY SIMILARITY).

SUBGULT: HOMODIMER OF HETERODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear:

SUBCELLULAR LOCATION: Nuclear:

BEVELOPMENTAL STAGE: IT IS SYNTHESIZED DURING OGGENESIS AND DEVELOPMENTAL STAGE: IT IS SYNTHESIZED DURING DORBHES AND PERSISTS IN THE CLEAVING EMBRYO AT AFFROXIMATELY CONSTANT LEVELS UNTIL IT IS DESPACED JUST REFORE GASTRULATION.

SUMALIRITY: SELDANDE JUST REFORE GASTRULATION.

LOMAIN: COMPOSED OF THREE COMMAINS. A MODULATING U-TERMINAL DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE REFERROR FAMILY.

NR2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytopiasmic (By similarity).
SIMILARITY: BELONGS TO THE EUKAPYOTIC RELEASE FACTOR 1 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (translation) in response to the termination codons UAA, UAG UGA (By similarity). SUBUNIT: HETERODIMER OF TWO SUBUNITS, ONE OF WHICH BINDS GTF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
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and for commercial
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright if is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions or its
                                                                                                                                                                                                                                                                                                                                                                                              MUPD_TREPA STANDARD: PRT: 532 AA 083873; 083873; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 47, Last annotation update) 15-JUN-2002 (Pel. 41, Last annotation update) (EC 6.3.2.9) (UDF-N-acettylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDF-N-acettylmuramoyl-L-alanyi-D-glutamate synthetase) (P-glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PR00398; STEDHORMONER.
PRINTS: PR00047; STEOIDEINGER
Procom PD000035; Znf_C4steroid: 1
                                                                                                                        MEDLINE-98272770: PubMed=9665876:

Fraser C.M., Norris S.J., Weinstork G.M., White O., Sutton G.G.,

Praser C.M., Norris S.J., Weinstork P., Fetchum K.A.,

Podson B., Gwild M., Hickey E.K., "layron P., Fetchum K.A.,

Sodergren E., Hardhum T.M., McLood M.P., Salzherg S., Peterson J.,

Sodergren E., Hardhum T.M., McLood M.P., Salzherg S., Peterson J.,

Sodergren E., Hardhum T.M., McLood M.P., Salzherg S., Peterson J.,

Schalak H., Bichardson D., Howell R., Childman M.D., Fulli C., Garland S.,

McDonald L., Artiach P., Rowman C., Otton M.D., Fulli C., Garland S.,

Hatch B., Horst K., Roberts K. Suchusky M., Weldman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00430; HOLI;
SMART; SM00399; ZnF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00104; hormone_rec; 1
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sit.ch).
                  Spirochete.";
Sylonop 281-35-388(1998).
FUNCTION: CELL WALL FORMATION CATALYZES THE ADDITION OF DEGLITAMATE TO THE NUCLEOTIDE PRECURSOR UDP-N-ACETYLMURAMOYL-L-
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                           Preponema pallidum.
Bacteria: Spirochaetales, Spirochaetaceac, Treponema
                                                                                                                                                                                                                                                                                                                                                                MURD OR TP0903
                                                                                                                                                                                                                                                                                                                                                                                 adding enzyme)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART: SM00399; ZnF_C4; 1.
PROSITE; PS00031; NHCLEAR_RECEPTOR: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T01360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                       STRAIN-Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger; Multigene family.
                                                                                                         Venter J.C.
                                                                                        "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 LESYT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LESYT 5
ALANINE (UMA) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 100.0%; Score 25: DB
Similarity 100.0%; Pred No 66;
5; Conservative 0; Mismutches
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236
470 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGAN: BINDING (BY SIMILARITY).; DD1:172Dc53CF3A5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR RECEPTOR-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532
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                                                                                                                                             Garland S.,
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S70_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                  HSP70 gene.";
J. Biol. Chem
                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a linense agreement (See http://www.ish-sib-sh-announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08. Last sequence update)
01-FEB-1994 (Rel. 28. Last annotation update)
Heat shock 70 kba protein (HSP70).
                                                                       PIR: A25646; A25646.
HSSP: P08109: 1CKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)
Eukaryota, Metazca, Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bilinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
Pfam; PF00012; HSP70; 1.
PRINTS: PR00301: HEATSHOCK70
                                                                                                                                                                                      or send an email to licensedisb-sib.ch)
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                J. BIOI. Chem. 261:12692-12699(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86304452; PubMed-3017985; Morimoto R.I., Hunt C., Huang S.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01225; Mur_ligase, Pfam; PF02875; Mur_ligase_C
TIGRFAMs: TIGP01087; murD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISE-PROT entry is oppyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation .
                                                InterPro: IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Organization, nucleotide sequence, and transcription of the chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9031,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E08106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS70_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidoglycan synthesis: Ceil wall; Cell division: Ligase: ATP-binding: Complete proteome.
ATP-binding: Complete proteome.
ATP-binding: Tomplete proteome.
ATP (POTENTIAL).
SEQUENCE 532 AA: 57847 MW; 3FD70557484778410 CF664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR004101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 LESYT 389
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                                                                                                                                   J02579; AAA48825.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata: Craniata: Vertebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%: Score 25; DB
100.0%; Pred. No. 76;
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O1:007:1996 (Rel. 34, Created)
O1:007:1996 (Rel. 34, Last sequence update)
15:7UN:2002 (Fel. 41, Last annotation update)
Heat shock-related 70 kma protein / (Heat shock 70 kma protein 2)
                                                                                                                                                                                                                                                        entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-s.b.ch).
                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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BonnyCastle L.L.C., Yu C.-E., Hunt T.R., Trask B.J., Clancy K.P.
Weber J.L., Patterson D., Schellerterg G.D.;
"Cloning, sequencing, and mapping of the human chromosome 14 heat
shock protein_gene (HSPA2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom: PD000089; Hsp70; 1.

PROSITE: PS00297; Hsp70_1; 1.

PROSITE: PS00329; Hsp70_3; 1.

PROSITE: PS01036; Hsp70_3; 1.

ATP-binding: Heat shock; Multigene family seguence 634 AA: 69750 MW: 427:FFF68D.
                                                                                                                                                                                      EMBL; L26336; AAA52698.1; -. EMBL; U56725; AAD11466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poux A.-F., Nguyen V.T.T., Squire L.A., Cox D.W.;
"A heat shock gene at 14922; mappil, and expression.";
"Hum. Mol. Genet. 3:1819-1822(1994).
-!- FUNCTION: IN COOPERATION WITH-THEP CHAPEPONES, HSP70S STABILIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Cransota, Vertebrata, Euteleostomi
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-126 FROM N.A. MEDLINE-95152505, PubMed-7849706,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goralski T.J., Krensky A.M.;
Submitted (APR-1996) to the EMBL/Wearank/DDBT databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID 9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROPHOBIC CHARACTER EXPOSED BY POLYPERFIDES DURING TRANSLATION OF POLICIAINS, STRESS-INDUCED DAMAGE SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER PROTEINS. THEY BIND EXTITUDED PEPTIDE SEGMENTS WITH A NET OTHER PROTEINS.
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EMBL, 010149, HSSP; P19120;

3HSC

U56725; AAD11466.1; -. U10149; AAC50076.1; -. HGNC:5235; HSFA2. 1PR001023; Hsp70

MIM: 140560; Genew;

InterProj

FF00012: HSP70; 1

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                                                                                                                                                  Shiral M. Hirakawa H. Kimoro M. Tabuchi M. Kishi F. Ouchi K. Shiba T. Ishii K. Hattori M. Kubara S. Nakazawa T.:
Shiba T. Ishii K. Hattori M. Kubara S. Nakazawa T.:
Shiba T. Ishii K. Hattori M. Kubara S. Nakazawa T.:
"Comparison of whole genome sequences of Chlamydia pneumoniae 3138 from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314 (2009).
Nucleic Acids Res. 28:2311-2314 (2009).
THE FUNCTION. PECOGNIZES A SPECIFIC HAIPDIN SEQUENCE ON PHIX SEDNA THIS STRUCTUPE IS THEN PECOGNIZED AND BOUND BY PROTEINS PRIB AND PRIC. FORMATION OF THE PRIMOSOME PROCEEDIS WITH THE SUBSEQUENT ACTIONS OF DNAB. DNAC, DNAT AND PETHASE PRIM THEN FUNCTIONS AS A HELICASE WITHIN THE PRIMOSOME (BY SIMILARITY).
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ProDom: PD000089; Hsp70: 1.
PP0STIE: PS00247 Hsp70: 1: 1
PR0STIE: PS00329; HSP70.2: 1.
PR0STIE: PS01036: HSP70.3: 1.
This SWISS-PFGT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bicinformatics Institute. There are restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a library agreement (See http://www.isb-sib.ch/aurounde/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White C., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S., Winher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Neison M., DeRey R., Folonay J., McClarty G., Salrberg S.L. Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0926\(\tilde{Y}\)2: 09JQA8: 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Primosomal protein N' (Replication factor Y). PRIA OR CPN0924 OR CPN092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding: Chaperone: Heat shock: Multigene family. CONFLICT 54 MISSING (IN PEF 3).

SEQUENCE 640 AA: 70021 MW: 3861755494E7B729 CPC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria: Chlamydiales: Chlamydiaceae: Chlamydo
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia preumoniae AR39.", % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) ^{2}
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100.0%; Pred. No. 94;
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation—the European Ricinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is no removed. Usage by and for commercial printitles requires a license agreement (Sec Mit) [www.isb-sil.ch.co.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MoPn / Nigg;
MEDLINE=20150255; PubMed=10684935;
Peed T D _ Brunham P C _ Shen C _
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Primosomal protein N' (Replication factor Y).
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Eisen J., Fraser C.M.
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Bacteria: Chlamydiales: Chlamydiacone: Chlamydia
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DNA replication: DNA-binding; ATP-oboding; Helicase; Primosome;
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SMART: SM00487; DFXDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequences of Chlamydia trachomatis MoPa and Chlamydia pneumoniae AR39.";
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InterPro: IPR001410; DEAD.
InterPro: IFR001650; Helicase_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIA OF TC0159
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                                                    TIGR;
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PEINCILIN: PRINCIPLY A SECTE "HARIPPIN SEMERAGE ON PHIX SSUNA. FINALLIN: PRINCIPLY A SECTE "HARIPPIN SEMERAGE ON PHIX SSUNA. THE STRUCTURE IS THEN PROCEINS AND BOUNT BY PROTEINS PRIB AND PRIC. FORMATION OF THE PRINCIPLE PROCEEDS WITH THE SUBSEQUENT ACTIONS OF LNAB, DNAT AND PRIMASE, PILA THEN FUNCTIONS AS A HELICASE WITHIN THE PRINCIPLE HELICASE MITHIN THE PRINCIPLE HELICASE THE PRINCIPLE HELICASE FAMILY.
                                                  TC0159;
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                                                                            AF002283; AAF39035.1;
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similarity 100.0%;
5; conservative (
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Hickey E.K., Peterson J. Uiterback T. Ryk, Bass S.,
Weldman T. Khouri H., Graven B., Rowman C. Dodson R.,
Nelson W., DeBoy R., Kolanay J., McClarty G., Salzbord S.L.,
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497
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C4-TYPE (POTENTIAL).
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DEEH ROX.
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Pred No 1 le+02;
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Primosomal protein N' (Replication factor Y).
PRIA OR CT778.
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                           ZN_FING
                                                                                                                                                  PTAM: PF00271; helicase_C: 1.
SMART: SMOO487: DEXPC: 1.
SMART: SM00490; HELICC: 1.
TIGREAMS: TIGROUS95; priA: 1.
DNA replication: DNA-binding: ATP-binding; Helicase: Primosome:
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.i-licele.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiamydia trachomatis.")
Science 282:754-759(1998).
Science 282:754-759(1998).
-:- FUNCTION: RECOGNIZES A SPECIFIC HAIRPIN SEQUENCE ON PHIX SSDNA
-:- FUNCTION: RECOGNIZES THEN RECOGNIZED AND BOUND BY PROTEINS PRIB AND
PRIC. FORMATION OF THE FELDINGSOME PROCEEDS WITH THE SUBSEQUENT
ACTIONS OF DNAB, DNAC, DNAT AND PRIMASEDS PRIA THEN FUNCTIONS AS A
HELICASE WITHIN THE PRIMOSOME (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE HELICASE FAMILY. PRIA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=D/UW-3/Cx: PubMed=9784136;
MEDLINE=99000005: PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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InterPro; IPR001650; Helicase_C.
InterPro; IPR005259; PriA.
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001350: AAC68373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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Query Match 100.0%; Score _5; DB 1; Length 753; Best Local Similarity 100.0%; Fred. No. 1.1e-02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gdps Qy 1 LESYT 5 Db 379 LESYT 383
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# SUMMARIES

	SCOLE	Match	Match Length DB	80	ID	Description
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	32	88.9	204	ς; W	ABP38988	Staphylococcus epi
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#### ALICNMENTS

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ID AAT4
Noncological degenerative disease PIV-1 envelope protein: qp120; taxio powers accessory glial cell otherwhine viral infection; powers with death, or ophal path, or opportunity memory loss; dementia, depression, psychosis, opportunity in faction;
                                                                                                                                                                                                                                                                                  HIV:1 gp120 indused neutrinal sell death inhibiting peptide #2.
                                                                                                                                                                                                neurotoxicity; inflammatory neurological disease; multiple sclerosis; tropical spastic paraparesis; Alzheimer's disease.
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        WPI; 1999-633695/54.
                                Pert C, Ruff M;
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of gr
                                                                                         ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The sc epidermidis sequences have antibacterial activity and can be used in yene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life
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cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1958,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY49695 and AAY49696 represent peptides which inhibit HIV-1 gp120 induced neuronal cell death. Pharmaceutical compositions containing the
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                                                                                                                                                                                                                                                                                                                                                                            Disclosure: SEQ ID 3833: 267pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI: 2002-381255/41
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IKEYFTS 7
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es 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermidis, open reading frame, OFF, kapterial infection, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-055779P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-064964P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Matches 5; Conserv
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                                           hybridisation assays, and are used to inhibit expression of the protein, is as antisense molecules for treatment of tumours, particularly those of high metastatic potential. Cells that have been modified so that they no longer produce the protein are used to produce NeuSGC-free glycoconjugates for therapeutic use. The DNA encoding the protein is used to produce recombinant protein and detection of the gene, normally durmant, can be used to diagnose tomours. Glycoproteins that lack NeuSGC mure closely resemble human products and are suitable for long term therapy since they contain no non-contain epitopes (NeuSGC-containing
                                                                                                                                                                                        The present sequence represents a new isolated protein cytidine monophospho-N-acetylneuramic acid hydroxylase, which is uncontaminated by cytochrome b5 or cytochrome b5 reductase. The protein is produced by exogenous DNA in prokaryotic or eukaryotic cells and it catalyses conversion of CMP NewSort to CMP-NewSort and NewSort which hybridise to DNA approximation acid respectively). Oligomyclectides which hybridise to DNA approximation acid respectively) to detect such myolele acids by
                                                                                                                                                                                                                                                                                                                                                                           New CMP:N-acetyl-neuraminic acid hydroxylase and related DNA - used esp. to delete enzyme activity in mammalian cells, allowing product of glycosprotein(s) without N-glycosyl-neuraminic acid suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1995;
07-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMP-NeuSAc hydroxylase; CMP-NeuSGo hydroxylase; enzyme activity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytidine monophospho-N-acetylneuramic acid hydroxylase
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Sequence
                                                                                                                                                                                                                                                                                                                              Claim 2; Page 32-33; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BOEF ) BOFHFINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 VKFYFTA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-119055/11.
                                  are immunogenic in humans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honold K. Kelm S. Schauer R. Schlenzka W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.98;
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Pred. No 97;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Query Match

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DB 18; Length 422;

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                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW10735 represents a parcine cytidine mano phosphate (CMF) Nacetyl-neuraminic acid (CMP-Neu5Ac) hydroxylase enzyme. The enzyme catalyses the conversion of CMP-Neu5Ac to CMP-Neu5Cc (Cytidine monophosphate-Neu1Ac to CMP-Neu5Cc (cytidine monophosphate-Neu1Ac to CMP-Neu5Cc (cytidine monophosphate-Neu1Ac to CMP-Neu5Cc (cytidine monophosphate-Neu1Ac this cFNA sequence are used for the production of CMP-Neu5Ac hydroxylase-deficient mammalian cells. The modified cells are useful for the production of recombinant glyyoproteins lacking Neu3pycoloyheuraminic acid side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-acetyl-neuraminic acid; Neu5ac; sialic acid; porcine; CMP; cytidine monophosphate; antisense therapy; recombinant production; N-glycoloylneuraminic acid side chain deficient; erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pornine CMP-N-acetyl-neuraminic acid hydroxylase - catalyses conversion of CMP-Neu5Ac to CMP-Neu5Gc, anti-sense sequences of DNA encoding CMP-N-acetyl-neuraminic acid hydroxylase are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW10735 standard: Protein: 422 AA
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                         ABP26246;
                                                                        ABP26246 standard; Protein; 728 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      chains, e.g erythropoietim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prodn. of modified glyco:proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine CMP-N-acetyl-neuraminic acid hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 IKEYFT 308
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                                                                                                                                                                                                                                                                                            Local Similarity
Wes 6: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         422 AA:
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                                                                                                                                                                                                                                                                               98.9%; _;
100.0%; _pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0:
                                                                                                                                                                                                                                                                                                                Score 32: DB 18;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlenzka W;
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                                                                                                                                                                                                                                                                                                                                         Length 422;
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                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus that is prevented or invated may be moringitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography. Immunoassays. and Itstheadship.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptuduceus/GBS (Streptuduceus administrate) of group A streptuduceus/GAS (Streptuduceus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have autibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the manufacture of medicaments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-00%-2000; 20000GR-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GH-0005640;
S cerevisiae apoptosis associated protein YIL112W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to abtermine whether a compound binds to biological sample. (1) is a nucleic acid encoding (1), may be (1). A composition complishing (1) or a nucleic acid encoding (1) may be used as a vaccine or diagnostic composition. The disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 3318; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-352536/38.
N-PSDB; ABN66877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polypeptide SEQ ID NO 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002 (first entry)
                                        27-JUL-2001
                                                                                                                    AAG70745 standard; Protein; 1460 AA
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus hacteria, such as meningitis, and for detecting a compound that binds to the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-001-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for detecting a compound that binds to the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telford J, Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the treatment of prevention of infortion or disease caused by
                                                                                                                                                                                                                   131 VKDYFTS 137
                                                                                                                                                                                                                                                       1 IKEYFIS 7
                                                                                                                                                                                                                                                                                                                                                                            728 AA;
                                                                                                                                                                                                                                                                                                Conservative
                                      (first entry)
                                                                                                                                                                                                                                                                                                                   88.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                   _score 32, DB 23;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grandi G,
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                                                                                                                                                                                                                                                                                                                                       Length 728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    may be
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3ULT 7
J29339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and neurodegeneration. The proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast and tungal nucleds acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungui infections, or for preventing apoptosis in certain diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast: fungus: apoptosis: infection, proliferative disease, vaccine; autoimmune disease: ischaemia; neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU29339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU29339 standard: Protein: 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1190 LKEYYTS 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1: 218pp: English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-357042/35.
N-PSDB; AAH29781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JANC ) JANSSEN PHARM NV
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Levy SB,
                                                                                                                                           08-MAR-2001; 2001W0-US07478
                                                                                                                                                                                                                                       W0200170776-A2
                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                   mar regulated polypeptide; NIMR: microbial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                 Novel mar regulated protein (NIMR) #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001 (first entry)
                                             (TUFT ) TUFTS COLLEGE
                                                                                              10-MAR-2000: 2000US-188362P
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5; Conserv
Barbosa TM,
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Reekmans RJ;
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71.4%;
  Alekshun MN
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Pred. No. le+03;
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RESULT 8
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a surface, and the virulence of a microbe in a surface, and the virulence of a microbe in a surface, and the virulence of a microbe in a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe on a surface, and the virulence of a microbe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound \dot{}
The present invention describes a carified or isolated macheic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in ARBI202 to AABBL194. Where expression of the macheic acid in a microorganism is capable of inhibiting proliferation of a microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                Novel nucleic acids encoding proteins required for Escherichia coliproliferation, useful for screening for antimicrobial agents - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli; identification; proliferation; microorganism; antimicrobial, antibacterial; antibiotic; gene therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia culi protein sequence ED; ID NO:424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG98376 standard; Protein; 150 AA
                                                                                                                     Claim 19; Page 544; 596pp; English
                                                                                                                                                                                                                                      N-PSDB; AAH81432.
                                                                                                                                                                                                                                                                                                              Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2000: 2000WO-US34419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial growth inhibition.
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                                                                                                                                                                                                                                                                                                            Ohlsen KL,
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                                                                                                                                                                                                                                                                                                                 Zyskind
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(I) have antibacterial and antiblotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism, and the manufactured antiblotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial protein to proliferation can be used as antisense therapeutics for killing bacteria. It additions to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid protess complementary to proliferation required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical species to hadellies to AAG94431, and AAB91486 to AAAB91486 to AAAB914
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25-FEB 1995
05-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAP 1999
01-APP 1999
01-APP 1999
01-APP 1999
16-APP 1999
16-APP 1999
23-APR 1999
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                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO. 52616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
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les 5; Conser
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99US-0123548.
99US-0125788.
99US-0125264.
99US-0126785.
              990S-0130077
990S-0130410
990S-0130510
990S-0131449
990S-0131449
990S-0132407
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9905-0128234.
9905-0128714.
9905-0129845.
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    29-JUN-1999;
30-JUN-1999;
01-JUL-1999;
01-JUL-1999;
02-JUL-1999;
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14-MAY-1999;
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20-MAY-1999;
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61-JUN-1999;
63-JUN-1999;
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24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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15-JUL-1999:
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9905-0135629
9905-0136021.
9905-0136392.
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99US-0134370.
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qqrrs-0139456.
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99US-0138094.
99US-0138540.
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99US-0140354.
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9905-0137502
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9905-0144005
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99US-0142055
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27-JUL-1999 28-JUL-1999 02-AUG-1999 02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999

9908-0147038. 9908-0147204. 9908-0147302. 9908-0147192.

99US-0145951. 99US-0146386. 99US-0146388.

990S-0145919

9908-0146389

9908-0145276. 9908-0145276. 9908-0145913. 9908-0145918.

16-AUG-1999; 17-AUG-1990

13-AUG-1999;

99US-0148341. 99US-0148565.

-1999 -1999;

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990S-0147493 990S-0147416 990S-0147493 990S-0147493 990S-0147935 990S-0148171 990S-0148319

20-AUG-1999; 23-AUG-1999;

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20 - AUG 18-AUG-1999;

-1999;

990S-0148684 990S-0149456 990S-0149426 990S-0149722 990S-0149723 990S-0149723 990S-0149992 990S-0149930

25

27-AUG-1999 27-AUG-1999 26-AUG-1999 27-AUG-1999

07-SEP

990S-01512823 990S-0151066 990S-0151066 990S-015108 990S-015103 990S-015128 990S-01528 990S-01528 990S-01530 990S-01530 990S-015403 990S-015403

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RESULT 10
ABB53504
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                         Query Match 83.3%; Score (), DB 23; Best Local Similarity 85.7%; Fred. No. 4.6e+02; Matches 6, Conservative 0, Mismatches 1
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25-007-1944
25-007-1944
25-007-1949
26-007-1949
26-007-1949
28-007-1944
28-007-1944
28-007-1944
28-007-1944
                                                                                                       The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB3300-ABB55621). The nucleic acid sequence is useful in the Jackettim and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this particular sacial action of communication of yogurt and cheese. Note: The sequence data for this particular is based on equivalent patent words: The sequence data for this particular is based on equivalent patent format directly from WIFO at ftp.wip.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lantococcus lactis protein rgpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB53504 standard; Protein; 402
                                                                                  Sequence
                                                                                                                                                                                                                                                                                  Claim 6; SEQ ID No 206; 2504pp; French.
                                                                                                                                                                                                                                                                                                                          New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                Bolotine A, Sorokine A, Renault F. Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AFR-2000: 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                                                                           lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 LKEYFSS
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  1 IKEYFTS 7
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5; Conserv
                                                                                    402 AA;
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9908-0161405

9908-0161406

9908-0161359

9908-0161360

9908-0161361

9908-016192

9908-016192

9908-016192
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71.48;
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Pred. No. 3e+02;
2; Mismatches
                                                      DB 23; Length 402;
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24-SEP-1999; 28-SEP-1999; 29-SEP-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999;

20-SEP-1999; 22-SEP-1999;

99US-0154779 99US-0155139

16-SEP-1999 15-SEP-1999 13-SEP-1999 10-SEP-1999

23-SEP-1999

99US-0155486. 99US-0155659. 99US-0156458.

06-00T-1999 07-00T-1999

-0157865

08-00T-1999; 12-00T-1999; 13-00T-1999; 13-00T-1999;

990S-0158232 990S-0158369 9905-0158029 -8066

14-00T-1999; 14-00T-1999;

13-OCT-1999

9908-0159294. 9908-0159295. 9908-0159329. 9908-0159330.

14 -OCT

-1999;

14-0CT

4-0CT-1999; 4-0CT-1999; 8-0CT-1999;

21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 22-0CT-1999

0;

99US-0159331 99US-0159584 99US-0159584 99US-0160761 99US-0160767 99US-0160770 99US-0160770 99US-0160815 99US-0160815

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ESULT 11
BB92997
D ABB92
X ABB92
X ABB92
X ABB92
X ABB97
X ABB
(ESULT 12

.BB91466

.D ABB91

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB92997 standard; Protein; 573 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 2208: 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidally active polypeptide SEQ ID NO 2208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2002 (first entry)
Arabidopsis thaliana
                                                                  Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                 ABB91466 standard; Protein: 598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 2002-259010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tietjen K. Weidler M:
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                                                                                                                             Herbicidally active polypeptide SEQ ID NO 677.
                                                                                                                                                                                                   31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 IKEYLTS 175
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Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 573;
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RESULT 13
ABB63300
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and compraining nucleic act of sequences from plant with nucleic actd or amino acid sequences from plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most shullar non-plant sequences are selected the polyphylides of nucleic acids encoding them are useful for identifying modularors. The identified modulators are
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                                                                                                                                                                                                                                                                                                                                            Drosophila, developmental blology well signalling insectibides
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WPT; 2001-656860/75.
N-PSDB; ABL07403.
                                                     Venter JC,
                                                                                      (PEKE ) PE CORP NY.
                                                                                                                          23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                     27-SEP-2001.
                                                                                                                                                                                                                                                       WC200171042-A2
                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                  brosophila melanogaster polypeptide SEQ ID NO 16692.
                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB63300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 677; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising aligning and comparing a cleic acid or amino acid sequences from non-plant from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing while acid of amino acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001WC-EP09892
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                                                                                                                                                                            23-MAR-1001; 1001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identify'\psi_A target proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weidler M;
                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%,
85.7%;
                                                     Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 23;
Pred No. 6.8e+02;
0; Mismatches 1
                                                       Myors EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a coleic acid or amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Length 598;
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New isolated reclete and detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Disclosure: SEQ ID NO 16692; 21pp + Sequence Listing; English.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016-ABL30511), expressed DNA sequences (ABL10176) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipu.int/pub/published\_pct\_sequences.

Sequence 762 AA:

Drosophila melanoyaster polypoptide SEQ ID NO 31140

26-MAR-2002 (first entry)

Drosophila: developmental biology, cell signalling: insecticide, pharmaceutical.

Drosophila melanogaster.

WU200171042-A2

27-SEP-2001

23-MAR-2001; 2001Wo-US09231.

23-MAR-2000: 2000US-191637P 11-JUL-2000: 2000US-0614150

(PEKE ) PE CORP NY

Venter JC, Adams M, Li PWD, Myers EW:

WPI; 2001-555550,75 N-PSDB; ABL12219.

New isolated morbely and detention reagent for detecting 1900 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Disclosure: SEQ ID NO 31140: 21pp + Sequence Listing: English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

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SS SS SS SX SX
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ABG15393
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          disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG10377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO _{\rm S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences (ABL01840-ABL16175) and the encoded proteins (ABB5773-ABB72072).
                                                                                                                                                                                                                       polypeptide (II) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCP) primers, cligomers, and for chromosome and grow and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tays for identifying expressed genes. (1) is useful in gene therapy technique for identifying expressed genes.
                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders on other traits and to assess biodiversity.
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diagnostic amino acid sequences of the invention
                                                                                                                          (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its buding partners are useful in medical imaging of sites expressing (II). (1) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 45752; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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23-ANG-2000; 200008-6649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene ma;ping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #15:84.
                                                                                                                                                                                                         for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 IFEYFTS 421
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85.7%;
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C Note: The sequence data for this patent did not appear in the printed C specification, but was obtained in electronic format directly from WIPO C at ftp.wipo inf/pub/published_pot_sequences.

X Sequence 1028 AA;

Q Sequence 1028 AA;

Query Match 83.3%; Score 30; DB 22; Length 1028; Best Local Similarity 71.4%; Pred. No. 1.1e+03; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 IKEYPTS 7
1::[1] b 454 IRGYPTS 460

earch completed: April 8, 2003, 12:01:40

ob time : 64.5667 secs
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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263956 mus sp. fib	11 063956	54	100.0	25	<b>-</b>
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#### ALI :NMENTS

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Q63956
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Overy Match 100.0%, Score 25: DB 11, Length 54; Best Local Similarity 100.0%; Pred No. 33; Matches 5: Conservative 0: Microstohes 0: Indels
                                             Q63956;
Q63956;
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                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Create!)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                     SEDIENTE
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craclata, Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciu i ignathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                     Fibrillin-1 (Fragment).
                                                                                                                                                                                              TISSUE=LIVER;
MEDLINE=94140368; PubMod=8307578;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    NCBI_TaxID=10095;
                                                                                                                                                                            Francke U.;
                                                                                                                                                                                   Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
                                      54 54
54 AA: 5707 MW;
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                       RA4A : ARAGRATICZA CRC64;
                                                                                                                                                                                                                                                                                                                                     PRT;
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 Gaps
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17 LESYT 21

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z318:
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Monocyte chemoattractant protein-3 (MCP-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9TTQ2
                                                                             Asano K., Nakamura M., Cyuma T., Fukunaga K., Matsubara H., Ishizaka A., Yamaguchi K., Kanazawa M.;
"Differential expression of CC chemokines in guinea pig lungs an allergic inflammation.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; A801340; BAA36456.1;
HSSP; P51671; IECT.
                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).

Bukaryota; Metazoa, Chordata; Cianlata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: AJ251190: CAB61626.1; -.
HSSP: P13500: IDOK.
ToterPro: IPP001811: Chemokine_IL8
Pfam: PF00049: IL8: 1.
SMART: SM00199: SCY: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-DEC-2001 (TrEMBLrel 19 Tast annotation update)
         InterPro: IPR000427; CC_chemkine_sml.
InterPro: IPR001811; Chemokine_IL8.
Pfam: PF00048; IL8; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of equine chemokines estaxin, monocyte chemoattractant profein (MCP)-1. MCP-2 and MCP-4. mRNA expression in tissues an induction by IL-4 in dermal fibroblasts."

Vet. Immunol. Immunopathol. 76:283-298(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21061912: PubMed=11044560
Benarafa C., Cunningham F.M., Hami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monocyte chemoattractant protein-2 precursor (Fragment).
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                                                                                                                                                                                                                                               TISSUE-LUNG
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SMART: SMOUL99: SCY: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Cunningham F.M., Hamblin A.S., Horohov D.W.,
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ilarity 100.0%;
Conservative 0
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BY SIMILARITY
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Pred. No. 52;
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Best Local :
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Best Local :
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                                                                                                                                                           Q9CWC7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
24.0150007Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-2115.

MEDIINE-2115.4947: PubMed-11677608:

MEDIINE-2115.4947: PubMed-11677608:

Parkhill J. Grugan S. James K. T. Thomson N. B. Fickard D., Wain J. Churcher C., Mungall K.L., Bentley S. D., Holden M.T.G., Sebaihia M., Bakker S., Basham D., Brooks K., Chillingworth T., Connerton P., Bakker S., Parkis P., Davies P. M., Inwed L., White N., Farrar J., Cronin A., Davis P., Davies P. M., Inwed L., White N., Farrar J., Cronin A., Davis P., Davies P. M., Inwed L., White N., Farrar C., Guarli M., Hutherford K., Simmonds M., Skeiton J., Stevens K., Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last athotation update)
SEQUENCE FROM N.A. STPAIDS THE CELLS: STPAIDS TO THE CELLS: MEDITINE-21085660; PubMed-11217851; Kawai J., Shinagawa A., Shibata K., Yoshino M., Arakawa T., Hara A., Fukunishi Y., Kouno H., Ad-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple drug resistant Salmonella enterior serrovar Typhi CTIA";
Nature 413:848-862(2001)
EMBL: AL513384; CAD09995.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00472; SMALL_CYTOKINES_COSEQUENCE 97 AA; 11159 MW; E169A
                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Cran ata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein HCM2.0128.
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                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                   Q9CWC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Plasmid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CT18
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                                                                                                                                                        241015000781K.
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AA;
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                   FRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilbdz MW;
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                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB
Pred. No. 67;
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB
Pred. No. 64;
                                                                                                                                                                                                                                                   *PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E189A17C165C2421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
82CA:3D5DB07760D CRC64;
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   Konno H., Adachi J., Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                            0;
                 Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                              Indels
   Ishii Y.,
Fukuda S.,
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                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gassferland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojinga N., Carninol P., de Bonaldo M.F., Blake J., Boffelli D., Rojinga N., Carninol P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinolch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustinolch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustinolch S., Fingwaid M., Fodfiquez T., Sakamoto N., Sasaki H., Sato K., Scheedrach G., Seya T., Shibata Y., Stiech K.-F., Sysaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker G., Wilming L., Wynshaw-Roris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayasahiraki Y.
                                                                                                                                                                                                                    Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Gaarrett P.A., Ragan M.A., Sensen C.M., Van der Oost J.;
The complete general of the stream theon Sulf likes sulfattiins P2., Proc. Natl. Acad. Sci. U.S.A. 98:7845-7849(2001).
BMBL: AE006683: ANXA0852.1;
InterPro: IPR0C2878; DUF35.
Pfam: PF01796; DUF35.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9UWT7,
01-MAY-2000 (TrEMBLrel. 13, Greated)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein SSO0532,
SSO0537 OF OFF 072_019
Sulfolobus solfatarious.
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC WIGHT, CRM LCTT, CR.
MEDLINE-2192296; PubMed+11427726;
She Q. Singh P. K. Confalonieri E. Zivanovic Y., Allard G.,
Awayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng
Thi-Ngon H.P., Redder P., Scheck M.E., Theriauit C., Telstrup N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
EMBL: AK019136: BAB31563.1; -.
MGD: MGI:1925497: 2410150007R1K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UWT7
                                                                                                                                                          ProDom; PD033834; DUF35; 1.
Hypothetical protein; Complete
SEQUENCE 133 AA: 14937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzawa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y mater
Local Similarity 100.0%; Score 25;
Local Similarity 100.0%; Pred. No.
hes 5; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 LESYT 102
56 LESYI 60
                                      1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K. Izawa M. Nishi K. Kiyosawa H., Kondo S., Yamanaka
, Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cienarchaeota, Theimopiotel, Sulfolobales, Sulfolobaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14901 MW; CBFFBFF76AC76AC4 CRC64;
                                                                                                  100.0%: Score 25; DB
100.0%: Pred. No. 91;
                                                                                                                                                                 proteome.
7A6E83EECD3DA8E7 CRC64;
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                                                                                 Mismatches
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                                                                                                                        DB 17: Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Saito R.,
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Db
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Best Local :
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Q9578:
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last substation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last substation update)
Hyportherical 18 4 kDa protein.
Macker fascicularis (Crab eating mecaque) (Cynomolgus monkey).
Erkaryota Metazua Cheriata, Cian'iia, Vertebrata, Euteleoston
Mammalia; Eutheria; Primates; Catarihini; Cercopithecidae;
Cercopithecinae, Macada.
                                                                                                                                                                                                        MEDLINE-20083487, FubMed=10617197.

Lin X., Kaul S., Rounsley S.D., Shoa T.P., Henito M.-I., Town C.D., Fujii C.Y., Mason T.M., Rowman C.I., Harnstead M.E., Feldblyum T.V., Fujii C.Y., Mason T.M., Rowman C.I., Harnstead M.E., Feldblyum T.V., Fujii C.Y., Mason T.M., Rowman C.I., Harnstead M.E., Feldblyum T.V., Farris F. Illimayam L., Talion L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Adams M.D., Fraser C.M., Venter J.C.;

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cross).

Bukaryota: Viridiplantae: Strept 1978. Embryophyta: Tracheophyta:

Strept 1974. Manuall-phyta 2001. Tylestus och exitoris Freid

eurosids II: Brassicales: Brassica wae: Arabidopsis.

NCBI_TaxID=4702:
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01-NOV-1998 (TrEMBLrel, 08, Last sequence update)
01-MAE-2002 (TrEMBLrel, 20, Last con tation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APG-2001) to the EMPL/Conkerk/DERT databases EMBL: AR070111; BAB63056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             080992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein: SEQUENCE 172 AA: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84L'560
Interpro: IPR000916; Bet_v_I. pfam. pr00407; Bet_v_I; 1.
                                    EMBL; AC004747; AAC31232.1; -.
                                                                    S.Retinod (MARY2000) to the EMRID edges TIPT databases.
-1- SIMILARITY: BELONGS TO THE BEINT FAMILY OF FATHOGENESIS-RELATED
                                                                                            Submitted (MAR-2000) to the BMB1
                                                                                                                Lin X.;
                                                                                                                                  STRAIN-CV.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                          Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                            STPAIN=CV
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               At2g26040 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolation of rowel full length of \Delta A elones from macagne testis cDNA libraries.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hashimato K., Osada N., Hida M., Fosoda J., Tanuma R., Hirai M.,
Terao K., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LESYT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LESYT 5
                                                          PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                          COLUMBIA;
                                                                                                                                  COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18393 MW; DEF TINCREBDEDBC4 CRC64;
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100.0%; Fred: No. 1.2c+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 172;
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STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G. Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus scifataricus F2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
EMBL, AE006676; AAK40756.1;
EMBL, AE006675; Hamilp_like; 1.
Pfam, PF01725; Hamilp_like; 1.
PfcpDom; PD004952; Hamilp_like, 1.
PTCPEAMA: T18900045; Hamilp_like, 1.
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Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                             SULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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01-OCT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pathogenesis-related protein.
SEQUENCE 190 AA; 21282 MW; CBB16E64BE2B8164 CRC54;
                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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                                                                                                                                                                                          Bacillus lichemiformis.
Bacteria: Firmioutes: Bacillus/Glostridium group: Bacillales
                                                                                                                                                                                                                                                                                                                                                                  050233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus solfatarious
                                             MEDLINE=96421969; PubMed=8824586
                                                                         STRAIN-FD50;
                                                                                                SEQUENCE FROM N.A
                                                                                                                                            NCBI_TaxID=1402;
                                                                                                                                                                        Bacillaceae:
                                                                                                                                                                                                                                             Putative siama-B regulator.
Yand X., Kang C.M., Brody M.S., Price C.W.:
"Opposing pairs of serine protein kinases and phosphatases transmit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 LESYT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 LESYT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                        Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21919 MW; A153E5AE08837F54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%: Score 25: DB 17: 100.0%: Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 10; 100.0%; Fred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     £1,6,18
1,8,18
1,8,18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    マスピ、
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 190,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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В

147 LESYT 151

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Query Match
Best Local Similarity
5, Conserve
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Q8ZS45
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                                                                                  Query Match
Best Local
                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8ZS45:
01:MAR-2002 (TrEMBLrel. 20, Created)
01:MAR-2002 (TrEMBLrel. 20, Last sequence update)
01:JUN-2002 (TrEMBLrel. 21, Last amotation update)
Hypothetical protein Air7667
ALR7667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 212:111:118(1998).
EMBL: AF034567; AAC29511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97323402; PubMed=9179850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signals of environmental stress to activate a bacterial transcription
                                                                                                                                                                                                               DNA Res. 8:205-213(2001).
EMBL, AP003602; BAB77310.1;
InterPro; IPP001982; Endonu-_LAG/HWH.
InterPro; IPR001005; Myb_DNA_binding.
FROSITE; PS00037; MYB_1; UNKNOWN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21595285; FubMed-11759840;
Kaneko T., Nakamura Y., Welk C.P., Kiritz T
Watanabe A., Iriquchi M., Ishikawa A., Kawas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor sigmaB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brody M.S., Price C.W.; Bacillus licheniformis sigB operon encoding the general stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98326316; PubMed=9661670; 
Brody M.S., Price C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FD50
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                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid p007120beta
Bacteria: Cyanobacteria: Nostonalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8ZS45
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                                                                                                                                                                                              Plasmid
                                                                                                                                                                                                                                                                                                                                              cyanobacterium Anabaena sp. strain PCC 7120.":
                                                                                                                                                                                                                                                                                                                                                                              Yasuda M., Tabata S.;
"Complete genomic sequence of the Hilamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LESYT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LESYT 5
     1 LESYT 5
                                                        Similarity
5; Conserv
                                                                                                                                                                 Hypothetical protein; Complete proteome. 216 AA; 25607 MW; A3F GD10B1E555B3 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001932; PP2C-like
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                                                                                                                                                              216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7120beta.
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Conservative (
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (strain PCC 7120).
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                                                                                  100.0%; Score 25; DR 16; 100.0%; Pred No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218/2307A5A12CE9 CRC64;
                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawashima K., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                 DB 16: Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasamoto S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 199;
                                                              Indels
                                                                 9
                                                              Saps
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Query Match:
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q43479;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                      Kawarabayasi Y. Himo Y. Horikawa H., Yamazaki S., Haikawa Jin-no K. Takabashi M. Sekine M. Baba S.T. Ankai A. Ko Hosoyama A. Fukui S. Nagai Y. Nishijima K. Nakazawa H. Takamiya M. Masuda S., Funahashi T. Tanaka T. Kudoh Y., Yamazaki J., Kushida N. Guuchi A. Aoki K.-I. Kubota K. Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (ITEMBLIEL 12, Created)
01-NOV-1999 (TIEMBLIEL 12, Last sequence update)
01-MAP-2002 (TIEMBLIEL), Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR001025; BAH. Interpro: IPR000561; EGF-like. Interpro: IPR000561; EGF-HD. Interpro: IPR001965; Znf_PHD. pfam; PF01426; BAH: 1. Pfam; PF00628; PHD: 1.
         EMBL: AP000064: BAA81535 1; -.
Interpro: IPR004361: Glyoxalase_1.
Interpro: IPR004360: Gly_bleo_diox.
Pfam: PF00903: Glyoxalase: 1.
                                                                                                                                                                                                                                          Desulfurococcaceae: Aeropyrum.
NCBI_TaxID=56636:
                                                                                                                                                                                                                                                                   Aeropyrum pernix.
Archaea, Crematchaeota: Thermoprotei; Desulfutococcales:
                                                                                                                                                                                                                                                                                                                                                                                  Q9Y8W5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART: SMO04/9: BAH: 1.
SMART: SMO04/9: PHD: 1.
PPOSTTE: PSO1186: EGE 2: "UKKUDWN_1.
SEQUEPHOF 227 AA 25741 MU POTABASASA472E24 OFOS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare (Barley).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ES43 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            043479
                                                                 orenarchaech, Aeropyrum pernix Ki.";
DNA Res. 6:83-101(1999),
                                                                                                                                                                                       MEDLINE-99310344; PubMed-10382955;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Hypothetical protein APE2519.
                                                                                                                                                                                                                                                                                                                                                                    09Y8W5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             steriod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4513;
PROSITE; PS00934; GLYOXALASE_I_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A barley cDNA clone with homology to the DNA binding domain of
                                                                                          "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LESYT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               od hormone receptors.";
sci. 106:91-98(1995).
X77575; CAA54682.]: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DBG576; TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01,
20,
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fred No. 1.7e+02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                235 AA
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  Q8SQT9
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel, 10, Created)
01-MAY-1999 (TrEMBLrel, 10, Last sequence update)
01-JUN-2902 (TrEMBLrel, 21, Last sencitation update)
Hypothetical 25.6 kDa protein.
          STRAIN-GB-M1;
STRAIN-GB-M1;
MEDLINE-21576510; PubMed-11719806:
                                                                                                                                                                                                                   08S0T9;
01-JUN-2002 (TrEMBLIE)
01-UN-2002 (TrEMBLIE)
01-UN-2002 (***EMBLIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Chemotaxis is essential for viriltors in Heliophacter pylori: 13-0.111 at the Chee of the Chee and Chey domains."

Steeling (Author) to the EMEL/Consequence databases.

EMBL: AF021091: AAD01686.1; A
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Jackson C.J., Pittman M.S., Clayton C.L., McColm A.A., Bagshaw J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome. SEQUENCE 235 AA; 25812 MW; 058/IA98DBE154A1 CRC64;
                                                                                                                                                            Encephaliterenn cuniculi.
Enkaryota: Microsporidia: Unikaryonidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ZIQ7;
01-MAY-1999 (TrEMBirel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ZIQ7
                                                                                                          STRAIN-GB-M1;
                                                                                                                                                 NCBI_TaxID=6035;
                                                                                                                                                                                            ECU11_1430
                                                                                                                                                                                                      DIPHTIN synthase
                                                                                                                                                                                                                                                                          Q8SQT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR004844; M-ppestrase.
InterPro: IPR004844; S/T_phosphtse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-NCTC 11637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria: Proteobacteria: epsilon wholivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori).
Ratinka M.D., Duprat S., Cornillot F., Motenier G., Thomarat F. Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker
                                                      SEQUENCE FROM N.A.
                                                                                                                        SECTIFNOF FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 LESYT 211
                                                                                whalthed (AFR-2001, or
                                                                                                                                                                                                                                                                                                                                                                                                   local similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                         1 LESYT 5
                                                                                                                                                                                                                                                                                                                                             2 LESYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
EMBL; AL590450: CAD260531; -.
SEQUENCE 262 AA; 29114 MW; CBACCA95ElDFD051 CPC64;
SEQUENCE 262 AA; 29114 MW; CBACCA95ElDFD051 CPC64;
Juery Match
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#### SUMMARIES

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#### ALIGNMENTS

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Lykke-Andersen J., Shu M.-D., Steltz J.A.;
"Human Upf protelns target an mRNA for nonsense-mediated decay when bound downstream of a termination codon.";
Cell 103:1121-1131(2000).
EMBL; AV013249; AAA048509 1; -.
InterPro; IPR003890; IF_EIF4G.
Pram; PP02854; MIF4G; 3.
SMART: SMO0543; MIF4G; 3.
SMART: SMO0543; MIF4G; 3.
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EMBL; AF301013; AAG33225.1; -.
EMBL; AF318574; AAG63699.1; -.
Interpro; IPR003890; IF_eIF4G.
Ptam; PF02854; MIF4G; 3.
SMART; SM00543; MIF4G; 3.
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Mendell J.T., Medghalchi S.M., Lake P.G., Noensie E N., Dietz H.C.;
Movel Upf2p Orthologues Suggest a Functional Link between Translation
Initiation and Nonsense Surveillance Complexes.";
Mol Cell Biol 20:8944-8957(2000)
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01-MAR-2001 (TEEMBLIP) 16. Last sequence update)
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Regulator of nonsense TRANSCRIPTS 2 (UPF2).
                                                                                                                                                                                                                                                                                                                                            saccharomyces cerevisiae upf2 protein and upf3 protein (Caenorhabditis
elegans SMG-4);";
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01-0CT-2000 (TrEMBLrel 15, Created)
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01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 27.2 kDa protein.
                                                                                                                                                                                              Yu J., Wang E., Hu X., Pang Y.;
Submitted (DEY-1000) to the EMBL, G. Ruck (DDBJ databases
EMBL: AF325155; AAL01783.1; -.
Hypothetical protein.
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Virology 287:391-404(2001).
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The complete sequences of 150 new cDNA clones from brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y., Yu J., Wang L., Hu X., Bac W., Li G., Chen C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1298 AA:
                                                                                                                                                                     11 protein.
            Conservative
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100.0%; FI
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85.78;
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                                             88.9%; Score 32;
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ding sequences of unidentified human genes.XVI
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Pred. No. 1.7e+02;
1: Mismatches (
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            Mismatches
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89;
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91 KEYFTS 96

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Mature 399:233-339(1999).

Nature 399:233-339(1999).

Nature AEO01691; AAD35134.1; -
Wilson R., Ainscoudh F., Anderson K., Baynes C., Berks M., Bonfield J. Burton J. Connell M. Copsey J. Copper J. Coulson A. Craxton M. Dear S., Du Z., Burbin P., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Liahtinita J., Lloyd C., McMurray A., Morthnore B., O'Callaghan M., Parcy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon M., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
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01-NOV-1999 (TrEMBLrel 12, Last segretore update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
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TIGP; TM0040; -.
InterPro; IPR000489
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                                                                                                                                                                  STRAIN-BRISTOL N2: MEDLINE-94150718: PubMed-7906398;
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NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
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Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CMP-N-acetylneuraminate monooxygenuse (EC 1.14.13.45) (Fragment).
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"The sequence of C. elegans cosmid *09H9.";
Schairted (IAN-1199) to the EMPL, **PATE, CDBJ databases
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"2.2 Mb of contiguous moderatide experies from chromosome III of
elegans.";
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ENCE   406 AA;   47500 MW;   580=00.173F4BFF79 CRP64;
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Matches 6
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Rawarabayasi Y. Hino Y. Horikawa H. Tin-no K. Takahashi M. Kawarabayasi Y. Baba S.-I. Ankai A. Kosugi H. Hosoyama A. Fukui S., Sekine M. Baba S.-I. Ankai A. Kosugi H. Hosoyama A. Fukui S., Nagai Y. Nishijima K. Otsuka R. Nakazawa H. Takamiya M. Kato Y. Nagai Y. Tanaka T. Kigoh Y. Yamazawa H. Takamiya M. Cauchi A. Yoshicawa T. Tanaka T. Kigoh Y. Yamazawa H. Yamaqishi A. Oshima T. Kikuchi H.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Y471;
01-NOV-1999 (TrEMBLrel 12,
01-NOV-1999 (TrEMBLrel 12,
01-NOV-1999 (TrEMBLrel 12,
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Hypothetical protein: Complete proteome.

SEQUENCE 479 AA; 54377 MW; 5C76E4E7151B5332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-JCM 10545 / 7:
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Sulfolobus tokodaii
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                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytidine monophosphate-N-acetylneuraminic acid hydroxylase
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Eukaryota: Metazoa: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMP-N-acetylneuraminic acid hydroxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                          Q9BTR8;
                                                                                                                                 Q9BTR8
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The molecular basis for the absence of N-Glycolylneuraminic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N A
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(CMP-N-acetylneuraminate monooxygenase).
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                                                                                                                                                                                                                                                 354 IKEYFT 359
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AP000985: BAB66241.1: -.
Pro; IPR000825; UPF0051.
                                                                                                                                                                                                                                                                                                                                                                                                                                  486 AA; 56508 MW; 1FB3BF498C1FA631 CRC64;
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                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             88.98; Score 32;
100.08; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.9%; Score 32; DB 17; Length 479; 100 0%; Pred. No. 1.7e+02;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stauffer R.L., Walker A., Ryder "Human and ape molecular clocks hypotheses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TERMBLED 20 Created)
01-MAR-2002 (TERMBLED 20, Last sempence update)
01-UNN-2002 (TERMBLED 21, Last annotation update)
CMP-N-acetylneuraminic acid hydroxylase (Fragment).
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                                                                                                                                                                                                                                                                                           Q9WV23; PPELIMINAPY:
Q9WV23;
Q1-NOV-1999 (TrEMBLrel 12,
Q1-NOV-1999 (TrEMBLrel 12,
Q1-DEC-2001 (TrEMBLrel 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pongo pygmaeus (Orangutan).
Rukaryota, Metazoa, Chordata; Granista: Vertebrata: Enteleostomi;
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                                                                                                                                                                                         Cricetulus griseus (Chinese hamste:).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Cricetinae;
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"CDNA sequence of CHO chah.";
Submitted (JUN-1999) to the EMBL/contrack/EERT databases.
                                                                                                                                     NCBI_TaxID-10029;
                                                                                                                                                                    Cricetulus.
                                                                                                                                                                                                                                                                            Cnah protein (Fragment)
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                                                         Goergen J.L., Chenu
                                                                                   SEQUENCE FROM N.A
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Pro; TPROO1281: Rieske
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497 AA,
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Conservative 0:
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100.0%; Pred. No. 1.8e+02;
hive 0; Mismatches 0
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100.0%; Pred. No. 1.8e+0
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PSULT 15
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C Q9TUJ
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Q9TUJ2: 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last amotation update)
SEQUENCE FROM N.A. ITTLE A., SUZUKİ A.; ITTLE A., SUZUKİ A.; "MOLECULAR EVOLUTION OF CMP-NeuAc hydoxylase in primates."; Submitted (MAY-1998) to the EMBL/ATHIBATIK/TURI databases. EMBL; AB013814; BAA86057.1; -. InterPro; IPR001281; Rieske.
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STRAIN-BALBYC: TISSUE-LIVER:
MEDLINE-95332362; PubMed-7608218;
MEDLINE-95332362; PubMed-7608218;
Kawano T., Koyama S., Takematsu H., Kozutsumi Y., Kawasaki H.,
Kawashima S., Kawasaki T., Suzuki A.;
Molecular cloning of cytidine monophospho-N-acetylneuraminic acid
hydroxylase.";
Mydroxylase.";
J. Biol. Chem. 270:16458-16463(1995).
EMBL; D21826; BAA04850.1;
MGD; MGI:103227; Cmah.
MGD; MGI:103227; Cmah.
MGD; MGI:103227; Cmah.
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Q61419;
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                                                                                                                                                                                                                         NCBI_TaxID-9544;
                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                CMP-N-acetylneuraminic acid hydroxylase. Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota: Metazoa: Chordata: Craniata; vertebiata; buteicoscome,
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CMAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMP-N-acetylneuraminic acid hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRŪŪ1281: Rieske.
Pfam; PF00355; Rieske; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ242835: CAB44648.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45% IKEYFT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 IKEYFT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IKEYFT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AA, 65105 MW; F62726BA5429359D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.4%: Score 32; DB 11; Length 577; 100.0%: Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.9%; Score 32; DB 11; Length 563; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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DR Pfam; PF00355; Rieske; 1.

SQ SEQUENCE 500 AA; 68256 MW; 3731054774A2908A95 CRC64;
QUETY Match
Best Local Similarity 100 0%; Proj. No. 2.1e+02;
Matches 6, Conservative 0; Rismatches 0; Indels 0; Gaps
OY 1 IKEYFT 6
[11] Db 458 IMEYFT 463
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Search completed: April 8, 2003, 12:04.17 Job time: 68.4167 secs